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cagcct gacatct gaag act ctgcggt ctatt tctgt gcaag ag tggt gacatat ag taact cttactgg tacttcg at gtctggggcacatat gaag act ctgcgggcacatat gaag act ctgaag act ctgcgggcacatat gaag act ctgaag act ctgcgggcacatat gaag act ctgaag act ctgaagggaccacggt caccgtctcttctgatcaatccaactctgaagaagcaaagaagaagaggaggccaaaaaggaggaagccaagaaatetaacagegtegacattgttetgacteagteteeageeaeeetgtetgtgaeteeaggagatagagtetetettteetgeagggee agccagagtattagcgactacttacactggtatcaacaaaaatcacatgagtetecaaggetteteatcaaatatgettecattcatc ggcggaggtgggtggcggateteagatecagttggtgcaatetggacetgagetgaagaagcetggagagacagt ggattggctggataaacaccccactctggagtgccaaaatatgtagaagacttcaaggacggtttgccttctcttttggaaacctctgccaacactgcatatttacagataagcaacctcaaagatgaggacacggctacgtatttctgtgtgagatccgggaatggtaactatga ${\tt cct} {\tt ggcct} {\tt act} {\tt tgt} {\tt act} {\tt ggggccaa} {\tt agggacact} {\tt ggtcact} {\tt gtct} {\tt ctg} {\tt act} {\tt aggagcccaa} {\tt act} {\tt ctg} {\tt act} {\tt act} {\tt ctg} {\tt act} {\tt act} {\tt act} {\tt ctg} {\tt act} {\tt act} {\tt ctg} {\tt act} {\tt act} {\tt ctg} {\tt act} {\tt$ ccaccgtccccagcacctgaactcctggggggatcgtcagtcttcctcttccccccaaaaacccaaggacaccctcatgatctcccg ggtg cata at gecaa gacaa aa geegg gg gg gg ag cag ta caa cag cac gt acc gt gg to a ge gt cet cac gg to cacaa gacaa ag cac gg gg gg gg gg gg gg ga gacaa cag cac gt acc gg to gacaa gacaacaa agg g cag c c c g aga ac cac ag g t g t a cac c c t g c c c cat c c g g g at g ag c t g ac cag g t cag c c t g ac c t g acgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacg cctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtct

<u>2H7-antiCD40 scFv MTH (SSS) MTCH2WTCH3</u> (2H7-40.2.220Ig) (amino acid sequence) (SEQ ID NO:___)

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY

QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKGGGGSGGGGSGGGGSSQAYLQQSGAELVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQSNSEEAK
KEEAKKEEAKKSNSVDIVLTQSPATLSVTPGDRVSLSCRASQSISDYLHWYQQKSH

ESPRLLIKYASHSISGIPSRFSGSGSGSDFTLSINSVEPEDVGIYYCQHGHSFPWTFGG
GTKLEIKRGGGGSGGGGSGGGGSQIQLVQSGPELKKPGETVRISCKASGYAFTTTG
MQWVQEMPGKGLKWIGWINTPLWSAKICRRLQGRFAFSLETSANTAYLQISNLKD

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EDTATYFCVRSGNGNYDLAYFAYWGQGTLVTVSDQEPKSSDKTHTSPPSPAPELL GGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTK PREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPRE PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSD GSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

<u>5B9 VH</u> (includes the VH leader peptide) (nucleotide sequence) (SEQ ID NO:___) atggctgtettggggctgetettetgeetggtgacattteeaagetgtgteetateecaggtgeagetgaageagteaggacetggcc tagtgeagteeteacagageetgteeateacetgeacagtetetggttteteattaactacetatgetgtacactgggttegecagtete caggaaagggtetggagtggagtggtggagtggtgggagtggatategaggtgggaateacagactataatgeagettteatatecagactgageate accaaggacgatteeaagagecaagttttetttaaaatgaacagtetgeaacetaatgacacagcatttattactgtgecagaaatg ggggtgataactaccttattactatgetatggactactggggteaaggaaceteagteacegteteetea

<u>5B9 VH</u> (minus the leader) (nucleotide sequence) (SEQ ID NO:___)

caggtgcagctgaagcagtcaggacctggcctagtgcagtcctcacagagcctgtccatcacctgcacagtctctggtttctcatta
actacctatgctgtacactgggttcgccagtctccaggaaagggtctggagtggtgggagtgatatggagtggtggaatcacaga
ctataatgcagctttcatatccagactgagcatcaccaaggacgattccaagagccaagttttctttaaaatgaacagtctgcaaccta
atgacacagccatttattactgtgccagaaatgggggtgataactacccttattactatgctatggactactggggtcaaggaacctca
gtcaccgtctcctca

20

<u>5B9 VH</u> (includes leader peptide) (amino acid sequence) (SEQ ID NO:___)

MAVLGLLFCLVTFPSCVLSQVQLKQSGPGLVQSSQSLSITCTVSGFSLTTYAVHWV

RQSPGKGLEWLGVIWSGGITDYNAAFISRLSITKDDSKSQVFFKMNSLQPNDTAIY

YCARNGGDNYPYYYAMDYWGQGTSVTVSS

25

<u>5B9 VH</u> (no leader peptide) (amino acid sequence) (SEQ ID NO:__)

QVQLKQSGPGLVQSSQSLSITCTVSGFSLTTYAVHWVRQSPGKGLEWLGVIWSGGI

TDYNAAFISRLSITKDDSKSQVFFKMNSLQPNDTAIYYCARNGGDNYPYYYAMDY

WGQGTSVTVSS

<u>5B9 VL</u> (nucleotide sequence) (SEQ ID NO:___)

atgaggttetetgeteagettetgggetgettgtgetetggatecetggatecactgeagatattgtgatgaegeaggetgeattete
eaateeagteactettggaacateagetteeateteetgeaggtetagtaagagteteetacatagtaatggeateacttatttgtattgg
tatetgeagaageeaggeeagteteeteageteetgatttateagatgteeaacettgeeteaggagteeagaaggteagtagga

5 gtgggteaggaaetgattteacaetgagaateageagagtggaggetgaggatgtgggtgtttattaetgtgeteaaaatetagaact
teegeteaegtteggtgetgggaeeaagetggagetgaaaegg

5B9 VL (amino acid sequence) (SEQ ID NO:___)

MRFSAQLLGLLVLWIPGSTADIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITY

LYWYLQKPGQSPQLLIYQMSNLASGVPDRFSSSGSGTDFTLRISRVEAEDVGVYYC

AQNLELPLTFGAGTKLELKR

5B9 scFv (nucleotide sequence) (SEQ ID NO:___)

25 <u>5B9 scFv</u> (amino acid sequence) (SEQ ID NO:)

30

MRFSAQLLGLLVLWIPGSTADIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITY LYWYLQKPGQSPQLLIYQMSNLASGVPDRFSSSGSGTDFTLRISRVEAEDVGVYYC AQNLELPLTFGAGTKLELKRGGGGSGGGGSGGGGSGQVQLKQSGPGLVQSSQSLS ITCTVSGFSLTTYAVHWVRQSPGKGLEWLGVIWSGGITDYNAAFISRLSITKDDSK SQVFFKMNSLQPNDTAIYYCARNGGDNYPYYYAMDYWGQGTSVTVSS

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<u>5B9 scFv-hmtIgG1-hCD80</u> (nucleotide sequence) (SEQ ID NO:___)

a agett g ceg ceat g aggtt ctet g ctet g g g ct g ctt g t g at ceet g g at ceat g cag at at t g t g at g ac g can a get t g c g at ceat g cag at at t g t g at g ac g can a g c t t g cag at a t t g t g at g ac g can a g c t t g cag at a t t g t g at g ac g can a g c t t g cag at a t t g t g at g cag at a t g cag at a t g at g cag at a t g cag atggctgcattctccaatccagtcactcttggaacatcagcttccatctcetgcaggtctagtaagagtctcctacatagtaatggcatca ctt att t g t at c t g c a g a a g c c a g c c a g c t c c t c a g c t c c t a g a t c t c a g a t c t c a g a t c t c a g a t t t a t c a g a t c t c a g a t c t c a g a t c t c a g a t t t a t c a g a t c t c a g a t c t c a g a t c t c a g a t c t c a g a t c t c a g a t c t c a g a t c t c a g a t c t c a g a t c c a g a tggttcagtagcagtgggtcaggaactgatttcacactgagaatcagcagagtggaggctgaggatgtgggtgtttattactgtgctc aaaatetagaactteegeteaegtteggtgetgggaceaagetggagetgaaaeggggtggeggtggetegggeggtggtggt cgggtggcggcggatcgtcacaggtgcagctgaagcagtcaggacctggcctagtgcagtcctcacagagcctgtccatcacct gcacagtctctggtttctcattaactacctatgctgtacactgggttcgccagtctccaggaaagggtctggagtggctgggagtgatatggagtggtggaatcacagactataatgcagctttcatatccagactgagcatcaccaaggacgattccaagagccaagttttctttaaaatgaacagtctgcaacctaatgacacagccatttattactgtgccagaaatgggggtgataactacccttattactatgctatgga ctactggggtcaaggaacctcagtcaccgtctcctctgatctggagcccaaatcttctgacaaaactcacacaagcccaccgagcc cagcacctgaactcctgggggggatcgtcagtcttcctcttcccccaaaaaccaaggacacctcatgatctcccggacccctgag gtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataat gccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggct gaatggcaaggagtacaagtgcaaggtetecaacaaageeeteecageeeecategagaaaaceateteeaaaggeaaaggge aaggettetateeeagegacategeegtggagtgggagageaatgggeageeggagaacaactacaagaceacgeeteegtg ctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctcegtgatgeatgaggetetgeacaaccactacaegeagaagageeteteeetgteteegggtaaageggateettegaacetgetee aggaggaatgagagttgagaagggaaagtgtacgcctgtataaatcgatactcgag

<u>5B9 scFv-hmtIgG1-hCD80</u> (amino acid sequence) (SEQ ID NO:

25 MRFSAQLLGLLVLWIPGSTADIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITY LYWYLQKPGQSPQLLIYQMSNLASGVPDRFSSSGSGTDFTLRISRVEAEDVGVYYC AQNLELPLTFGAGTKLELKRGGGGSGGGGSGGGGSSQVQLKQSGPGLVQSSQSLS ITCTVSGFSLTTYAVHWVRQSPGKGLEWLGVIWSGGITDYNAAFISRLSITKDDSK SQVFFKMNSLQPNDTAIYYCARNGGDNYPYYYAMDYWGQGTSVTVSSDLEPKSS 30 DKTHTSPPSPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP

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ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGKADPSNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRNERLRRESVRPV

<u>2e12 scFv WTH CH2 CH3</u> (2e12 scFv-WthIgG-CD80) (nucleotide sequence) (SEQ ID NO:)

a agettat gg att tt caa gt g cag att tt cag ette ct get a at cag t get cat a at gt cea gag gag te ga catt gt get caccea a tote cage ttett t gg ctg t g tote tagg te agag ge cae cate te ctg cag ag e cag t gaa ag t g t tag at at tat g te acaa g t tagg to the tagger of tagger of the tagger of taggerta at g cag t g g tacca a cag a a accag g a cag c cac c caa act cet cat c to t g cat c caa c g tag a at c t g g g t c cet g cet g cat cet g cataggttt agtggcagtgggtctgggacagactt cagcct caacat ccatcctgtggaggaggatgat at tgcaatgt at ttctgt cagccide accept the second content of the second content of10 aaagtaggaaggttccttggacgttcggtggaggcaccaagctggaaatcaaacggggtggcggtggctcgggcggaggtggctcgggtggcggcggatctcaggtgcagctgaaggagtcaggacctggcctggtggcgccctcacagagcctgtccatcacatgcaccgtctcagggttctcattaaccggctatggtgtaaactgggttcgccagcctccaggaaagggtctggagtggctgggaatgat atggggtgatggaagcacagactata att cagc to to a a atc cagactgag catcacca aggaca act coa agagc caa gttt to the contract of the coaaaaatgaa cag tot gcaaa ct gatgaca cag ccag at a ctact gt gccag agat gg ttatag taact tt cattact at gt tat gg action of the content of the c. 15 actggggt caaggaacct cagtcaccgtctcct cagatctggagcccaaatcttgtgacaaaactcacacatgcccaccgtgcccageacctgaactcctgggggggaccgteagtetteetetteeeceeaaaaeceaaggacacceteatgateteeeggacceetgaggt caagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcag 20 ggettetateceagegacategeegtggagtgggagageaatgggeageeggagaacaaetacaagaceaegeeteeegtget ggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggggaacgtcttctcatgctcc gtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaagcggatccttcgaacctgctccc 25 ggaggaatgagagattgagaagggaaagtgtacgcctgtataaatcgat

<u>2e12 scFv WTH CH2 CH3</u> (2e12 scFv-WthIgG-CD80) (amino acid sequence) (SEQ ID NO:___)

MDFQVQIFSFLLISASVIMSRGVDIVLTQSPASLAVSLGQRATISCRASESVEYYVTS
30 LMQWYQQKPGQPPKLLISAASNVESGVPARFSGSGSGTDFSLNIHPVEEDDIAMYF
CQQSRKVPWTFGGGTKLEIKRGGGGSGGGGGGGGGGQVQLKESGPGLVAPSQSLS
ITCTVSGFSLTGYGVNWVRQPPGKGLEWLGMIWGDGSTDYNSALKSRLSITKDNS

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KSQVFLKMNSLQTDDTARYYCARDGYSNFHYYVMDYWGQGTSVTVSSDLEPKS CDKTHTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFN WYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALP APIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ PENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSL SLSPGKADPSNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV

<u>2H7-human IgE Fc (CH2-CH3-CH4)</u> (nucleotide sequence) (SEQ ID NO: ____)

a agett g ceg ceatgg at ttt caagt g cag at ttt cagett cet g ctaat cag t get teag teata at t g ceag agga caa at t g t te teata at teag t g cagett caget g cagett caget g cagett g cagett g caget g cagett g caget g ccccag tete cag caate ct g tet g cate te cag g g g a g a a g g tea caat g a ct t g cag g g c cag e t caa g t g t a c g t g cae g ct caa g t g t a c g c g c c a g t e t ca g g g g c a g ct caa g t g t a c g c g c c a g t e t c c a g g g g a g a a g g t c a c a t g c a c t g c a g c c a g c t c a g g g g c a g c t c a g g g c c a g c t c a g g g g c a g c t c a g g g g c a g c t c a g g g g c a g c t c a g g g g c a g c t c a g g g g c a g c t c a g g g g c a g c t c a g g g g c c a g c t c a g c c a gggtaccagcagaagccaggatcctcccccaaaccctggatttatgccccatccaacctggcttctggagtcctgctcgcttcagtg g cagt gg g t ct gg g acctet ta cte te te a caat cage ag ag t gg ag get gaag at get ge caet tatta ct g ce ag t gg ag t tt acte te te te cae a cage ag t gg ag t tg ag ag t tg ag ag t tg agggagctctcaggcttatctacagcagtctggggctgagctggtgaggcctggggcctcagtgaagatgtcctgcaaggcttctggc taca catttac cag ttaca at at geactgg ta aag cag acacctag a cag gg cet gg aat gg at t gg ag ctatt tat ceag gaa at the cag gaacagcctgacatctgaagactctgcggtctatttctgtgcaagagtggtgtactatagtaactcttactggtacttcgatgtctggggcac agggaccaeggteaeegtetetgateaegtetgeteeagggaetteaeeeeggeeeaeegtgaagatettaeagtegteetgegaeg ggacggcaggtcatggacgtggacttgtccaccgcctctaccacgcaggagggtgagctggcctccacacaaaagcgagctcaeccteageeagaageactggetgteagaeegeaeetaeaeetgeeaggteaeetateaaggteaeaeetttgaggaeageaeeaa cacgat cacct g to tgg tgg tgg acct g g cacccag caag g g g acc g tg acct g acct g g tccc g g g cag t g g g acct g t cacgat cacct g tccc g g g cag t g g g acct g t cac g g t cac g g g cag t g g g acct g t cac g g t cac g g g cac g t g a c c t g acct g t cac g g t cac g g g cac g t g a c c t g acct g g t cac g g g c cag t g g a c c t ggaaccactccaccagaaaggaggagaagcagcgaatggcacgttaaccgtcacgtcacctgccggtgggcacccgagact cggcccgcgtgctgccccggaagtctatgcgtttgcgacgccggagtggccgggagccgggacaagcgcaccetcgcctgc ctgatecagaacttcatgeetgaggacateteggtgeagtggetgeacaaegaggtgeageteeeggaegeeeggeaeageaeg acgcagcccgcaagaccaagggctccggcttcttcgtcttcagccgcctggaggtgaccagggccgaatgggagcagaaaga aatctaga

2H7 scFv IgE (CH2-CH3-CH4) (amino acid sequence) (SEQ ID NO:__)

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY

QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS

FNPPTFGAGTKLELKGGGGSGGGGSGGGGSSQAYLQQSGAELVRPGASVKMSCK

5 ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS

TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSDHVCSRDFTP

PTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQE

GELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLSR

PSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLTV

10 TSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEWP

GSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRLE

VTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK

2H7 scFv MH (SSS) MCH2WTCH3 (nucleotide sequence) (SEQ ID NO:___)

15 aagettgeegecatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgttetet 🦿 cccag to tecage a at cet g to tecage g g agaa g g to a cast g cage g g ccage to a a g to tecage g g cage to a categories of the contract of the contract g can be a contract g can be aggtaccag cagaag c caggat cotcocccaa accet ggat ttat geoccate caacet gget to t ggag to cot get cagt gat the tage of the contraction of the contrageagtgggtetgggacctettaeteteaeaateageagagtggaggetgaagatgetgeeaettattaetgeeagtaggagttt taacceaccacgttcggtgctgggaccaagctggagctgaaagatggcggtggctcgggcggtggtggtctggaggaggtg 20 ggageteteaggettatetacageagtetggggetggtgaggetgggggeteagtgaagatgteetgeaaggettetgge tacacatttaccagttacaatatgcactgggtaaagcagacacctagacagggcctggaatggattggagctatttatccaggaaatgactattaccaggaaatgactaggattggagctattatccaggaaatgactaggactaggattggagctattatccaggaaatgacaggacaggacactggaatggattggagctattatccaggaaatgacagacaggacagacaggacagacaggacagacaggacagacggtgatactteetaeaateagaagtteaagggeaaggeeacaetgaetgtagaeaaateeteeageaeageetaeatgeageteag cagcctgacatctgaagactctgcggtctatttctgtgcaagagtggtgtactatagtaactcttactggtacttcgatgtctggggcac agggaccacggtcaccgtctcttctgatcaggagcccaaatcttctgacaaaactcacacatccccaccgtccccagcacctgaac 25 tectggggggatcgtcagtcttcctcttcccccaaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaag ccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaagga gtacaagtgcaaggtetecaacaaagcceteccagececcategagaaaacaatetecaaaggcaaagggcageceegagaac 30 cage gacateg cegt gg ag t gg gag ag caat gg ge ag ceg gag aa caacta caa gaccae ge ctee eg t gg actee gacae to gat gag ag tage ag caa t gag ag caa t caa t gag ag caa t caa t gag ag caa t gag ag caa t gag ag caa t gag ag caa t gag ag caa t caa t caa t gag ag caa t gag agggeteettetteetetacagcaageteacegtggacaagagcaggtggcagcaggggaacgtetteteatgeteegtgatgcatga ggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

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2H7 scFv MH (SSS) MCH2WTCH3 (amino acid sequence) (SEQ ID NO:___)

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
5 FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAELVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
THTSPPSPAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
10 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

5B9 scFv MTHWTCH2CH3 (nucleotide sequence) (SEQ ID NO:___)

aagettgeegecatgaggttetetgeteagettetggggetgettgtgetetggateeetggateeaetgeagatattgtgatgaegea ggetgeatteteeaateeagteaetettggaacateagetteeateteetgeaggtetagtaagagteteetaeatagtaatggeatea aaaatctagaacttccgctcacgttcggtgctgggaccaagctggagctgaaacggggtggcggtggctcgggcggtggtggt ${\tt cgggtggcggatcgtcacaggtgcagctgaagcagtcaggacctggcctagtgcagtcctcacagagcctgtccatcacct}$ gcacagtctctggtttctcattaactacctatgctgtacactgggttcgccagtctccaggaaagggtctggagtggctgggagtgat atggagtggtggaatcacagactataatgcagctttcatatccagactgagcatcaccaaggacgattccaagagccaagttttcttt aaaatgaacagtctgcaacctaatgacacagccatttattactgtgccagaaatgggggtgataactacccttattactatgctatgga ctactggggtcaaggaacctcagtcaccgtctcctctgatcaggagcccaaatcttctgacaaaactcacacactccccaccgtcccc ageacetgaacteetggggggacegteagtetteetetteeceecaaaaceeaaggacaceeteatgateteeeggaceeetgag gtcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataat gccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggct gaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaacaatctccaaagccaaagggc ${\tt ctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctc}$ cgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

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5B9 scFv MTHWTCH2CH3 (amino acid sequence) (SEQ ID NO:__)

MRFSAQLLGLLVLWIPGSTADIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITY
LYWYLQKPGQSPQLLIYQMSNLASGVPDRFSSSGSGTDFTLRISRVEAEDVGVYYC

AQNLELPLTFGAGTKLELKRGGGGSGGGSGGGGSSQVQLKQSGPGLVQSSQSLS
ITCTVSGFSLTTYAVHWVRQSPGKGLEWLGVIWSGGITDYNAAFISRLSITKDDSK
SQVFFKMNSLQPNDTAIYYCARNGGDNYPYYYAMDYWGQGTSVTVSSDQEPKSS
DKTHTSPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP
ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS
LSPGK

Human IgG1 hinge mutations

2H7 scFv- MTH (CSS) WTCH2CH3 (nucleotide sequence) (SEQ ID NO:___)

aagettgeegeeatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggacaaattgttetet 💛 cccagtetecageaateetgtetgeatetecaggggagaaggteacaatgaettgeagggeeageteaagtgtaagttacatgeact ggtaccagcagaagccaggatcctcccccaaaccetggatttatgccccatccaacetggcttctggagtcctgctcgcttcagtg geagtgggtetgggacetettaeteteacaateageagatggaggetgaagatgetgecaettattaetgecageagtggagttt cagcet gacatet gaagactet geggtet att tet gt geaagagt ggt gt act at a gt aactet taet ggt act te gat gt et gggeae en gede fan de gegen gegagggaccacggtcaccgtctcttctgatcaggagcccaaatcttgtgacaaaactcacacatccccaccgtccccagcacctgaac teetggggggaeegteagtetteetetteececcaaaaacceaaggaeacecteatgatcteeeggaeecetgaggteaeatgegtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaag gtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaacaatctccaaagccaaagggcagccccgagaac cagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgac

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2H7 scFv- MTH (CSS) WTCH2CH3 (amino acid sequence) (SEQ ID NO:___)

5 MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAELVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSCDK
10 THTSPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

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2H7 scFv- MTH (SCS) WTCH2CH3 (nucleotide sequence) (SEQ ID NO:___)

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cagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgac ggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcagggggaacgtcttctcatgctccgtgatgcatga ggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

5 2H7 scFv-MTH (SCS) WTCH2CH3 (amino acid sequence) (SEQ ID NO:__)
MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAELVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
10 TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
THTCPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
15 SPGK

2H7 scFv-MTH (SSC) WTCH2CH3 (nucleotide sequence) (SEQ ID NO:___)

cacaggtgtacaccctgccccatcccgggatgagctgaccaagaaccaggtcagcctgacctgctggtcaaaggcttctatcc
cagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgac
ggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatga
ggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

5

2H7 scFv- MTH (SSC) WTCH2CH3 (amino acid sequence) (SEQ ID NO:__)

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAELVRPGASVKMSCK

ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
THTSPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE

NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

HIgGMHcys1 (nucleotide sequence) (SEQ ID NO:___)

gtt gtt gat cag gag ccc aaa tct tct gac aaa act cac aca tg

20

HlgGMHcys2 (nucleotide sequence) (SEQ ID NO:___)

gtt gtt gat cag gag ccc aaa tct tgt gac aaa act cac aca tct cca ccg tgc

HIgGMHcys3 (nucleotide sequence) (SEQ ID NO:

25 gtt gtt gat cag gag ccc aaa tct tgt gac aaa act cac aca tgt cca ccg tcc cca gca cct

<u>HulgG1 MTCH3Y405</u> (nucleotide sequence) (SEQ ID NO:____)

 $gggcagccccgagaaccacaggtgtacaccctgcccccatcccgggaggagatgaccaagaaccaggtcagcctgacctgcct\\ ggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctc\\$

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 $ccgtgctggactccgacggctccttctacctctatagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctc\\ atgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtccccgggtaaatga$

HulgG1 MTCH3Y405 (amino acid sequence) (SEQ ID NO:___)

5 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFYLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

HulgG1 MTCH3A405 (nucleotide sequence) (SEQ ID NO:___)

HulgG1 MTCH3A405 (amino acid sequence) (SEQ ID NO: ___)

15 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFALYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

<u>HuIgG1 MTCH3A407</u> (nucleotide sequence) (SEQ ID NO:___)

Gggcagcccgagaaccacaggtgtacaccetgccccatccgggaggagatgaccaagaaccaggtcagcctgacctgcc
tggtcaaaggettctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcct
cccgtgctggactccgacggctcettcttcctcgccagcaagctcaccgtggacaagagagaggggaacgtcttct
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HuIgG1 MTCH3A407 (amino acid sequence) (SEQ ID NO: _)

25 GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLASKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

HulgG1 MTCH3Y405A407 (nucleotide sequence) (SEQ ID NO:___)

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gggcagccccgagaaccacaggtgtacaccctgccccatcccgggaggagatgaccaagaaccaggtcagcctgacctgcct ggtcaaaggettctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctc ccgtgctggactccgacggctccttctacctcgccagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctc atgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtccccgggtaaatga

5

<u>HulgG1 MTCH3Y405A407</u> (amino acid sequence) (SEQ ID NO:__)

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP

VLDSDGSFYLASKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

10 <u>HulgG1 MTCH3A405A407</u> (nucleotide sequence) (SEQ ID NO:___)

gggcagccccgagaaccacaggtgtacaccctgccccatcccgggaggagatgaccaagaaccaggtcagcctgacctgcct ggtcaaaggcttctatcccagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctc ccgtgctggactccgacggctccttcgccctcgccagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttct catgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtcccgggtaaatga

. . . 15

<u>HulgG1 MTCH3A405A407</u> (amino acid sequence) (SEQ ID NO:___)

GQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP

VLDSDGSFALASKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

20 2H7 scFv MTH (SSS) WTCH2MTCH3Y405 (nucleotide sequence) (SEQ ID NO:___)
aagettgeegecatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggacaaattgtteet
ceeagteteeageaateetgtetgeateteeaggggagaaagteacaatgaettgeagggeeageteaagtgtaagttaeatgeact
ggtaceageagaageeaggateeteeeeaaaceetggatttatgeeceateeaacetggettetggagteeetgetegetteagtg
geagtgggtetgggacetettaeteteteacaaateageagatggaggetgaagatgetgeeacttattaetgeeageagtggagttt
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30 agggaceacggteacegteetettetgateaggageeeaaatettetgaeaaaacteacacateeceacgteeceageacetgaac

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tcctggggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtg
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ccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaagga
gtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaaacaatctccaaagccaaagggcagcccgagaac
cacaggtgtacaccctgcccccatccgggaggagatgaccaagaaccaggtcagcctgacctgctggtcaaaggcttctatcc

ggctctgcacaaccactacacgcagaagagcctctccctgtccccgggtaaatgatctaga

2H7 scFv MTH (SSS) WTCH2MTCH3A405 (nucleotide sequence) (SEQ ID NO:___)
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ggctcttgcacaaccactacacgcagaagagcctctccctgtcccgggtaaatga

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2H7 scFv MTH (SSS) WTCH2MTCH3A405 (nucleotide sequence) (SEQ ID NO:___) mdfqvqifsfllisasviiargqivlsqspailsaspgekvtmtcrasssvsymhwyqqkpgsspkpwiyapsnlasgvparf sgsgsgtsysltisrveaedaatyycqqwsfnpptfgagtklelkdgggsggggggggggggggggggaqylqqsgaelvrpgasvkmsc kasgytftsynmhwvkqtprqglewigaiypgngdtsynqkfkgkatltvdkssstaymqlssltsedsavyfcarvvyysn sywyfdvwgtgtfvtvssdqepkssdkthtsppspapellggpsvflfppkpkdtlmisrtpevtcvvvdvshedpevkfnwyvdgvevhnaktkpreeqynstyrvvsvltvlhqdwlngkeykckvsnkalpapiektiskakgqprepqvytlppsreemt knqvsltclvkgfypsdiavewesngqpennykttppvldsdgsfalyskltvdksrwqqgnvfscsvmhealhnhytqksl

20 <u>2H7 scFv MTH (SSS) WTCH2MTCH3A407</u> (nucleotide sequence) (SEQ ID NO:___)

aagettgeegeeatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgtteete
ceeagteteeageaateetgetgeateteeaggggagaaaggteacaatgaettgeagggeeageteaagtgtaagttacatgeaet
ggtaceageagaageeaggateeteeeeaaaeeetggatttatgeeeeateeaaeetggettetggagteetgeetteagtg
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ggageteteaggettatetaeageagtetggggetgagetggtgaggeetggggeeteagtgaagatgteetgeaaggettetgge
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eageetgacatetgaagaetetgggtetatttetgtgeaagagtggtgtaetatagtaaetettaetggtaettegatgtegggeae
agggaceaeggteaeegtetettetgateaggageeeaaatettetgacaaaaeteaeacaeteeeacegteeeagaeetgaae
teetggggggaeegteagtetteetetteeeeeeaaaaeeeaaggaeaeecteatgateteeeggaeeeetgaggteaeatgegtg

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2H7 scFv MTH (SSS) WTCH2MTCH3A407 (amino acid sequence) (SEQ ID NO:__)

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY

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FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAELVRPGASVKMSCK

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THTSPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV

DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE

KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN

NYKTTPPVLDSDGSFFLASKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS

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2H7 scFv MTH (SSS) WTCH2MTCH3Y405A407 (nucleotide sequence) (SEQ ID NO:)

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2H7 scFv MTH (SSS) WTCH2MTCH3Y405A407 (amino acid sequence) (SEQ ID NO:)

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
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FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAELVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
THTSPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFYLASKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

2H7 scFv MTH (SSS) WTCH2MTCH3A405A407 (nucleotide sequence) (SEQ ID NO:___)

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2H7 scFv MTH (SSS) WTCH2MTCH3A405A407 (amino acid sequence) (SEQ ID

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAELVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
THTSPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSREEMTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFALASKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS

2H7 scFv MTH (SCC) WTCH2CH3 (nucleotide sequence)

aagettgeegeeatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgttetet eeeagteteeageaateetgetgeateteeagggagaaaggteacaatgaettgeagggeeageteaagtgtaagttaeatgeact ggtaceageagaageeaggateeteeeeaaaceetggatttatgeeeeateeaacetggettetggagteetgetgeteeggtggggttagggaeetettaeteteteacaateageagagtggaggetgaagatgetgeeacttattaetgeeageagtggagttt

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2H7 scFv MTH (SCC) WTCH2CH3 (amino acid sequence)

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGSSQAYLQQSGAELVRPGASVKMSCK
20 ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
THTCPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
25 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

2H7 scFv MTH (CSC) WTCH2CH3 (nucleotide sequence)

aagettgeegeeatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgttetet eecagteteeageaateetgtetgeateteeaggggagaaggteacaatgaettgeagggeeageteaagtgtaagttaeatgeact ggtaeeageaggageeaggateeteeeeaaaceetggatttatgeeeeateeaaeetggettetggagteeetgetgegteagtg

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g cagtgggtctgggacctcttactctctcacaatcagcagagtggaggctgaagatgctgccacttattactgccagcagtggagttttaacccaccacgttcggtgctgggaccaagctggagctgaaagatggcggtggctcgggcggtggtggtctggaggaggtg ggagetet caggettatet acage agtet gggget gaget ggggeet ggggeet cagt gaag at gteet geag gettet ggeet to get gaget the state of the stattaca catttac cagttaca at at geact gg sta a ag cag acacctag a cag gg catt gg a at gg at tg ga at tacacatt taccag ga a at tacacatt taccag ga at tacacat tacacatt taccag ga at tacacatt taccag ga at tacacat tacacat tacacatt taccag ga at tacacat tacaagggaccac ggt caccg tetett ctg at cag gag cccaa at ctt gtgacaa aact cac acc gtg ccca gcacct gaac accept a comparation of the comparation of theteefggggggacegtcagtetteetetteeeccaaaacccaaggacacecteatgateteeeggacecetgaggtcacatgegtg 10 ccgcggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaacaatctccaaagccaaagggcagccccgagaac cagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgac ggeteettetteetetacageaageteacegtggacaagageaggtggcagcaggggaacgtettetcatgeteegtgatgcatga 15 ggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

2H7 scFv MTH (CSC) WTCH2CH3 (amino acid sequence)

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
20 FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAELVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSCDK
THTSPPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
25 EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

2H7 scFv MTH (CCS) WTCH2CH3 (nucleotide sequence)

aagettgeegeeatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgttetet ceagteteeageaateetgtetgeateteeagggagaaggteacaatgaettgeagggeeageteaagtgtaagttaeatgeact

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g cagtgggtctgggacctcttactctctcacaatcagcagagtggaggctgaagatgctgcaccttattactgccagcagtggagtttta acceace acgt to get get gegace a aget gaa a gat gg c gg t gg c to g gg c gg t gg to g gat c t g ga gg ag g t g to get get get gg to get gg to get gat get gg to get gat get gg to get gat get gg to get gg to get gg to gg to get gg to gg to get gg to gg to get gg to gg to get gg to gg to get gg to gg to get gg to gg to get gg to gg to get gg to gg to gg to get gg to gg to gg to gg to get gg to gg to gg to gg to ggggagctctcaggcttatctacagcagtctggggctgagctggtgaggcctggggcctcagtgaagatgtcctgcaaggcttctggc taca catttac cagttaca at at geact gg sta a ag cag acacctag a cag gg cct gg a at gg at t gg ag ct at tt at ccag ga a at gg at the control of the control ofagggaccacggtcaccgtctcttctgatcaggagcccaaatcttgtgacaaaactcacacatgtccaccgtccccagcacctgaac tcctggggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtg gtggtggacgtgaggccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaagga gta caa gt gcaa g g to to caa caa a a g coctoc cag gccccat c g a gaa a a caa to to caa a g g caa a g caa a g g caa a g caa a g g caa a g g caa a gcage gacatege egg agateg gag age a at ggg cage egg agaacaacta caa gac cae geet ce gt get ggactee gacatege agatege gag agaacaacta caa gac cae geet gag agatege gag agaacaacta caa gac cae geet gga gag agaacta caa gac cae geet gag agaacta caa gac cae gac caggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

2H7 scFv MTH (CCS) WTCH2CH3 (amino acid sequence)

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY

20 QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAELVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSCDK
THTCPPSPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY

25 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

30 <u>HulgAHlgA-T4-ORF</u> (nucleotide sequence)

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ctgeacegaceggeectegaggacetgetettaggtteagaagegateeteaegtgeaeactgaceggeetgagagatgeeteag
gtgteacetteacetggacgeecteaagtgggaagagegetgtteaaggaceacetgacegtgacetetgtggetgetacagegtg
tecagtgteetgeegggetgtgeegagecatggaaceatgggaagacetteaettgeactgetgeetaceegagteeaagacee
egetaacegceaceeteteaaaateeggaaaceatteeggeeegaggteeacetgetgeegeegteggaggaggeece
tgaacgagetggtgacgetgacgtgeetggaacgtggetteageeeaaggatgtgetggttegetggetgeaggggteacagg
agetgeeeggagaagtacetgacttgggeateeeggeaggageeeageagggeaceaceaceacettegetgtgaceageata
etgegegtggcageegaggactggaagaagggggacacetteteetgcatggtgggecacgagggeetteae
acagaagaceategacegcttggeggtaaacecaccacetteteetgaatgtgtgtgtgtgaggggaggtggacgggateettega

HulgAHlgA-T4-ORF (amino acid sequence)

DQPVPSTPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEAILTCTLTGLRDASGV
TFTWTPSSGKSAVQGPPDRDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKT
PLTATLSKSGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQ
ELPREKYLTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAF
TQKTIDRLAGKPTHVNVSVVMAEVDADPSN

1D8-IgAH IgA-T4-CD80 (nucleotide sequence)

AA

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10 1D8 scFv IgAH IgA-T4-CD80 (amino acid sequence)

MDFQVQIFSFLLISASVIMSRGVDIVLTQSPTTIAASPGEKVTITCRASSSVSYMYWY
QQKSGASPKLWIYDTSKLASGVPNRFSGSGSGTSYSLAINTMETEDAATYYCQQW
SSTPLTFGSGTKLEIKRGGGGSGGGGSGGGGGGGGGGQVQLKEAGPGLVQPTQTLSLTCTV
SGFSLTSDGVHWIRQPPGKGLEWMGIIYYDGGTDYNSAIKSRLSISRDTSKSQVFLK
INSLQTDDTAMYYCARIHFDYWGQGVMVTVSSDQPVPSTPPTPSPSTPPTPSPSCC
HPRLSLHRPALEDLLLGSEAILTCTLTGLRDASGVTFTWTPSSGKSAVQGPPDRDL
CGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKSGNTFRPEVHLLPP
PSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLTWASRQEPSQGTTT
FAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLAGKPTHVNVSVVM
AEVDADPSNNLLPSWAITLISVNGIFVICCLTYCFAPRCRERRRNERLRRESVRPV

human IgE Fc (CH2-CH3-CH4) ORF (nucleotide sequence)

AA

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<u>human IgE Fc (CH2-CH3-CH4) ORF</u> (amino acid sequence)

DHVCSRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDV DLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSN PRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKE EKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPE VYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTK GSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGKADPS

1D8 scFv-human IgE Fc (CH2-CH3-CH4)-CD80 (nucleotide sequence)

a agettat ggatttte aget geagattte aget te ct get a at eagt get te aget cat a at get eagt aget the ag15 agtete caa caac cataget geatete cag ggg aga aggte accate acct geog tge cage te cag tg taa gt ta cat gt act ggt aggte accate acct geographic can get the cataget grant and the cataget grant graccag caga agte agge generocceta a act et gg at that gas a categorage the tagge generocceta and the tagge grant aggregation of tagge grant aggrgtgggtctgggacctcttattctctcgcaatcaacaccatggagactgaagatgctgccacttattactgtcagcagtggagtagtact gateteaggtgeagetgaaggaggeaggacetggeetggtgeaacegacacagacectgteceteacatgcactgteietgggtt 20 cacagatta ta atteag ca attaa at ceagact gag cateag cag ggaca cete caag ag cea ag ttt tettaa aa at caa cag tet gag cateag cateag cag gag cateag cateag cag gag cateag cateag cateag cag gag cateag cateag cag gag cateag ccaaactgatgacacagccatgtattactgtgccagaatccactttgattactggggccaaggagtcatggtcacagtctcctctgatc acgtot get ccagggact teacce ege ceacegt gaag at etta eagtegt et gegacggegggcact teecce ega ceat acgtot get can be a supported by the contract of the contrac25 ttgtccaccgcctctaccacgcaggagggtgagctggcctccacacaaagcgagctcaccctcagccagaagcactggctgtca gaccgcacctacacctgccaggtcacctatcaaggtcacacctttgaggacagcaccaagaagtgtgcagattccaacccgagag gggtgagcgcctacctaagccggcccagcccgttcgacctgttcatccgcaagtcgcccacgatcacctgtctggtggtggacct ggcacccagcaaggggaccgtgaacctgacctggtcccgggccagtgggaagcctgtgaaccactccaccagaaaggaggag aagcagcgcaatggcacgttaaccgtcacgtcacctgccggtgggcacccgagactggatcgagggggagacctaccagtg 30 cagggtgacccacccccacctgcccagggccctcatgcggtccacgaccaagaccagcggcccgcgtgctgccccggaagtctatgcgtttgcgacgccggagtggccggggagccgggacaagcgcaccctcgcctgatccagaacttcatgcctgaggac

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ateteggtgeagtgetgeacaacgaggtgeageteeeggacgeeeggeacageacgaegeageeegeaagaceaaggget eeggettettegtetteageegeetggaggtgaceagggeegaatgggageagaaagatgagtteatetgeegtgeagteeatga ggeagegageeeeteacagaeegteeagegageggtgtetgtaaateeeggtaaageggateettegaageteecateetggge eattaeettaateteagtaaatggaatttttgtgatatgetgeetgacetaetgetttgeeeeaagatgeagagagagaggaatg agagattgagaagggaaagtgtaegeeetgtataaategata

1D8-scFv-human IgE Fc (CH2-CH3-CH4)-CD80 (amino acid sequence)

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<u>5B9-IgAH IgA-T4-CD80</u> (nucleotide sequence)

<u>5B9-IgAH IgA-T4-CD80</u> (amino acid sequence)

MRFSAQLLGLLVLWIPGSTADIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITY
LYWYLQKPGQSPQLLIYQMSNLASGVPDRFSSSGSGTDFTLRISRVEAEDVGVYYC
AQNLELPL'IFGAGTKLELKRGGGGSGGGSGGGGSGQVQLKQSGPGLVQSSQSLS
ITCTVSGFSLTTYAVHWVRQSPGKGLEWLGVIWSGGITDYNAAFISRLSITKDDSK
SQVFFKMNSLQPNDTAIYYCARNGGDNYPYYYAMDYWGQGTSVTVSSDQPVPST
PPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEAILTCTLTGLRDASGVTFTWTPS
20 SGKSAVQGPPDRDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLS
KSGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKY
LTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDR
LAGKPTHVNVSVVMAEVDADPSNNLLPSWAITLISVNGIFVICCLTYCFAPRCRER
RRNERLRRESVRPV

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<u>5B9-scFv-human IgE Fc (CH2-CH3-CH4)-CD80</u> (nucleotide sequence)

aagettgeegeeatgaggttetetgeteagettetggggetgettgtgetetggateeetggateeaetgeagatattgtgatgaegea ggetgeatteteeaateeagteaetettggaaeateagetteeateteetgeaggtetagtaagagteteetaeatagtaatggeatea ettatttgtattggtatetgeaggaegeaggeeagteteeteageteetgatttateagatgteeaaeettgeeteaggagteeeagaea ggtteagtageagtgaggaeetgaggaaetgattteaeaetgagaateageagagtggaggetgaggatgtgggtgtttattaetgtgeteaaaatetagaaetteegeteeaegtteggtgetgggaeeaagetggagetgaaaeggggtggeggtggetegggeggtggtgggt

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cgggtggcggatcgtcacaggtgcagctgaagcagtcaggacctggcctagtgcagtcctcacagagcctgtccatcacctgcacagtctctggtttctcattaactacctatgctgtacactgggttcgccagtctccaggaaagggtctggagtggctgggagtgatatggagtggtagaat cacagactata atgcagcttt catatc cagactgag catcacca aggacgattc caagagc caagttt to title at the catataccagactgag and the catataccagactgag catcacca aggacgattc caagagc caagttt to title at the catataccagactgag catcacca aggacgattc caagagc caagttt to title at the catataccagactgag catcacca aggacg at the catataccagactgag catcaccagactgag catcacca aggacg at the catataccagactgag catcacca aggacg at the catataccagactgag catcaccagactgag catcaccagactctactggggtcaaggaacctcagtcaccgtctcctctgatcacgtctgctccagggacttcaccccggcccaccgtgaagatcttaca gtcgtcctgcgacggcggcggcacttccccccgaccatccagctcctgtgcctcgtctctgggtacaccccagggactatcaac ateacetggetggaggaegggeaggteatggaegtggaettgteeaeegeetetaeeaegeaggagggtgagetggeeteeaea caaagcgagctcaccctcagccagaagcactggctgtcagaccgcacctacacctgccaggtcacctatcaaggtcacacctttg aggacag caccaagaagt g t g cagattc caacccg ag aggg g t g agc g catacct a ag ccg g cccag ccc g t t c g acct g t t can be a significant of the contract of the contract g contract g acct g to the contract g conttecgea a g tege coe a constraint of the constrgtgggaagcctgtgaaccactccaccagaaaggaggagaagcagcgcaatggcacgttaaccgtcacgtcacctgccggtg egaccaagaccageggccegegtgetgecceggaagtetatgegtttgegaegeeggagtggceggggageegggaeaage gcaccctegcetgctgatccagaacttcatgcetgaggacateteggtgeagtggcacaaegaggtgcageteeeggacge ccggcacagcacgacgcagccccgcaagaccaagggctccggcttcttcgtcttcagccgcctggaggtgaccagggccgaat at cccggtaa ageggateette gaagetee cateet gggee at tacettaatet cagtaa at ggaattttt gtgat at get geet gaeet gaagetee gaa

20 <u>5B9-scFv-human IgE Fc (CH2-CH3-CH4)-CD80</u> (amino acid sequence)

MRFSAQLLGLLVLWIPGSTADIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITY
LYWYLQKPGQSPQLLIYQMSNLASGVPDRFSSSGSGTDFTLRISRVEAEDVGVYYC
AQNLELPLTFGAGTKLELKRGGGGSGGGGSGGGGSSQVQLKQSGPGLVQSSQSLS
ITCTVSGFSLTTYAVHWVRQSPGKGLEWLGVIWSGGITDYNAAFISRLSITKDDSK
SQVFFKMNSLQPNDTAIYYCARNGGDNYPYYYAMDYWGQGTSVTVSSDHVCSR
DFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTAS
TTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSA
YLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNG
TLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP
EWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFS
RLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGKADPSKLPSWAITLISV
NGIFVICCLTYCFAPRCRERRRNERLRRESVRPV

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<u>2e12-scFv-IgAH IgA-T4-CD80</u> (nucleotide sequence)

a agettat ggatttt caagt g cagatttt cagetteet getaat cagt gette agte at a at gte cagag gag te gae at t gte cae central gag to gae at the cagetteet get and the cagetteet gas to gat the cagetteet gat the cagetteet gas to gat the cagetteet gat ta a tote cage ttett t gg et g te totag g te agaga ge cace at et cet ge agage cag t gaa a g t g te agag te agtaatgcagtggtaccaacaggaaaccaggacagccacccaaactcctcatctctgctgcatccaacgtaggaatctggggtccctgcc aaagtaggaaggttccttggacgttcggtggaggcaccaagctggaaatcaaacggggtggcggtggctcgggcggaggtggg accgtctcagggttctcattaaccggctatggtgtaaactgggttcgccagcctccaggaaagggtctggagtggctgggaatgat atgggtgatggaagcacagactata att cagc to to a a at cagactgag catcaccaaggacaactccaagagccaagtt to the attack of the contract of tactggggl caaggaacct cagtcaccgtctcct cagatcagc cagttccct caactccacct accccact cacctacccc acctacccc acctaccc acctacccc acctaccc acctacccacctgaccgtgacctctgtggctgctacagcgtgtccagtgtcctgccgggctgtgccgagccatggaaccatgggaagaccttc acttgcactgctgcctaccccgagtccaagaccccgctaaccgccaccctctcaaaatccggaaacacattccggcccgaggtcc acetgctgcegcegcegteggaggagctggceetgaacgagctggtgacgctgacgtgcetggcacgtggcttcagccccaag gatgtgctggttcgctggctgcaggggtcacaggagctgcccggcgagaagtacctgacttgggcatcccggcaggagcccag 🧃 coaggeaccaccaccttegetgtgaccageatactgegegtggcagcegaggactggaagaagggggacacctteteetgeat § gttg tcatggcggaggtggacgcggatccttcgaacaacctgctcccatcctgggccattaccttaatctcagtaaatggaatttttgtgtataaatcgatac

25 2<u>e12-scFv-IgAH_IgA-T4-CD80</u> (amino acid sequence)

MDFQVQIFSFLLISASVIMSRGVDIVLTQSPASLAVSLGQRATISCRASESVEYYVTS
LMQWYQQKPGQPPKLLISAASNVESGVPARFSGSGSGTDFSLNIHPVEEDDIAMYF
CQQSRKVPWTFGGGTKLEIKRGGGGSGGGGGGGGGGGGGGGGQVQLKESGPGLVAPSQSLS
ITCTVSGFSLTGYGVNWVRQPPGKGLEWLGMIWGDGSTDYNSALKSRLSITKDNS
KSQVFLKMNSLQTDDTARYYCARDGYSNFHYYVMDYWGQGTSVTVSSDQPVPS
TPPTPSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEAILTCTLTGLRDASGVTFTWTP
SSGKSAVQGPPDRDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLS

KSGNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKY LTWASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDR LAGKPTHVNVSVVMAEVDADPSNNLLPSWAITLISVNGIFVICCLTYCFAPRCRER RRNERLRRESVRPV

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2e12-scFv-human IgE Fc (CH2-CH3-CH4)-CD80 (nucleotide sequence)

a agettat gg att ttc a agt gc ag att ttc agett cet gc ta at cag t get cat a t gt cca g ag gag t cg acat t g t get cac cet a t get at a t get cat a taateteeagettetttggetgtetetaggteagagageeaceateteetgeagageeagtgaaagtgttgaatattatgteaeaagtt taatgeagtggtaceaacagaaaceaggacagecacecaaactectcatetetgeatecaacgtagaatetggggteeetgee aaagtaggaaggttccttggacgttcggtggaggcaccaagctggaaatcaaacggggtggcggtggctcgggcggaggtggg togg st togg st constant a general state of the state oaccg to teagggt to teat taaccg get at ggt gt aa actg ggt te gee age ctc eaggaa ag gg to t gg ag t gg tag gat gat tag the same of the samatggggtgatggaagcacagactataattcagctctcaaatccagactgagcatcaccaaggacaactccaagagccaagttttctt aaaaatgaacagtctgcaaactgatgacacagccagatactactgtgccagagatggttatagtaactttcattactatgttatggact 🔯 actggggtcaaggaactcagtcaccgtctcctcagatcacgtctgctccagggacttcaccccgcccaccgtgaagatcttacag tegteetgegaeggegggegggaetteeccegaecateeageteetgtgeetegtetetgggtaeacceeagggaetateaaeat cacctggetggaggacggcaggteatggacgtggacttgtecaccgcctctaccacgcaggagggtgagctggcctccacac aaagcgagctcaccctcagccagaagcactggctgtcagaccgcacctacacctgccaggtcacctatcaaggtcacacctttga ccgcaagtcgccacgatcacctgtctggtggtggacctggcaccagcaaggggaccgtgaacctgacctggtcccgggcca gtgggaagcctgtgaaccactccaccagaaaggaggagaagcagcgcaatggcacgttaaccgtcacgtcacctgccggtg cgaccaagaccagcggcccgcgtgctgccccggaagtctatgcgtttgcgacgccggagtggccggggagccgggacaagc cegg cacag cac gac gac gac agac caa g g g ct ceg g ct tet te g tet teag ceg cet g g ag g t g ac cag g g ceg a at tet te g cet g cat g cac g g g ceg a at tet cap ceg cac g cat cccgg ta a agcgg at cetteg a agctece at cctggg ccattacet ta at ctcag ta a at gg a at titt gt gat at gct gcct gacct ta accept a acceptact gettt gecccaa gat geaga gaga gaga gaga gaga gaga ta gaga gag

MDFQVQIFSFLLISASVIMSRGVDIVLTQSPASLAVSLGQRATISCRASESVEYYVTS
LMQWYQQKPGQPPKLLISAASNVESGVPARFSGSGSGTDFSLNIHPVEEDDIAMYF
CQQSRKVPWTFGGGTKLEIKRGGGGSGGGGGGGGGGGGGGQVQLKESGPGLVAPSQSLS
ITCTVSGFSLTGYGVNWVRQPPGKGLEWLGMIWGDGSTDYNSALKSRLSITKDNS
5 KSQVFLKMNSLQTDDTARYYCARDGYSNFHYYVMDYWGQGTSVTVSSDHVCSR
DFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTAS
TTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSA
YLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNG
TLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATP
10 EWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFS
RLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGKADPSKLPSWAITLISV
NGIFVICCLTYCFAPRCRERRRNERLRRESVRPV

500A2 scFv (nucleotide sequence)

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500A2 scFv (amino acid sequence)

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NT

5' oligo:

Name : IgGWT3

 ${\tt GTTGTTTTCGAAGGATCCGCTTTACCCGGAGACAGGGAGAGGCTCTT}$

5 NT

3' oligo:

Name : hIgGWT5

GITGTTAGATCTGGAGCCCAAATCTTGTGACAAAACTCACACATG

NT

10 5' oligo:

Name : FADD5

Sequence

GTTGTGGATCCTTCGAACCCGTTCCTGGTGCTGCACTCGGTGTCG

NT

15 3' oligo:

Name : FADD3

Sequence

GTTGTTATCGATCTCGAGTTATCAGGACGCTTCGGAGGTAGATGCGTC

NT

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20 <u>FADD-CSSCFV</u> (nucleotide sequence)

30 <u>FADD-CSSCFV</u> (amino acid sequence)

VDPSNPFLVLLHSVSSSLSSSELTELKFLCLGRVGKRKLERVQSGLDLFSMLLEQND LEPGHTELLRELLASLRRHDLLRRVDDFEAGAAAGAAPGEEDLCAAFNVICDNVG KDWRRLARQLKVSDTKIDSIEDRYPRNLTERVRESLRIWKNTEKENATVAHLVGA LRSCQMNLVADLVQEVQQARDLQNRSGAMSPMSWNSDASTSEAS

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HCD28tm5B (nucleotide sequence)

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 ${\tt GTTGTGGATCCTCCCTTTTGGGTGCTGGTGGTGGTGGTGCTAT}$ ${\tt AGCTTG}$

10 <u>HCD28tm3S</u> (nucleotide sequence)

GTTGTTTCGAACCCAGAAAATAATAAAGGCCACTGTTACTAGCAAGCTATAGC AAGCCAG

HCD28tm5' (nucleotide sequence)

15 GTTGTGGATCCTCCCTTTTGGGTGCTGGTGGT

HCD28tm3' (nucleotide sequence)

GTTGTTTCGAACCCAGAAAATAATAAAGGCCAC

20 HCD80tm5' (nucleotide sequence)

GTTGTGGATCCTCCTGCTCCCATCCTGG

HCD80tm3' (nucleotide sequence)

25 GTTGTTTCGAACGGCAAAGCAGTAGGTCAGGC

MFADD5BB (nucleotide sequence)

GTTGTGGATCCTTCGAACCCATTCCTGGTGCTGCTGCACTCGCTG

MFADD3XC (nucleotide sequence)

GTTGTTATCGATCTCGAGTCAGGGTGTTTCTGAGGAAGACAC

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Murine FADD (amino acid sequence)

VDPSNMDPFLVLLHSLSGSLSGNDLMELKFLCRERVSKRKLERVQSGLDLFTVLLE QNDLERGHTGLLRELLASLRRHDLLQRLDDFEAGTATAAPPGEADLQVAFDIVCD NVGRDWKRLARELKVSEAKMDGIEEKYPRSLSERVRESLKVWKNAEKKNASVA GLVKALRTCRLNLVADLVEEAQESVSKSENMSPVLRDSTVSSSETP

MCASP3-5 (nucleotide sequence)

GTTGTGGATCCTTCGAACATGGAGAACAACAAAACCTCAGTGGATTCA

25 MCASP3-3 (nucleotide sequence)

GTTGTTATCGATCTCGAGCTAGTGATAAAAGTACAGTTCTTTCGT

MCASP8-5 (nucleotide sequence)

GTTGTTTCGAACATGGATTTCCAGAGTTGTCTTTATGCTATTGCTG

MCASP8-3 (nucleotide sequence)

GTTGTTATCGATCTCGAGTCATTAGGGAGGGAAGAAGAAGAGCTTCTTCCG

5 <u>hcasp3-5</u>(nucleotide sequence)

GTTGTGGATCCTTCGAACATGGAGAACACTGAAAACTCAGTGGAT

<u>hcasp3-3</u> (nucleotide sequence)

GTTGTTATCGATCTCGAGTTAGTGATAAAAATAGAGTTCTTTTGTGAG

10

<u>hcasp8-5</u> (nucleotide sequence)

GTTGTGGATCCTTCGAACATGGACTTCAGCAGAAATCTTTATGAT

<u>hcasp8-3</u> (nucleotide sequence)

15 GTTGTTATCGATGCATGCTCAATCAGAAGGGAAGACAAGTTTTTTCT

1. 2H7 scFv with alternative VHL11 mutations:

Nucleotide sequence

Aagettgeegeeatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgttete
teecagteteeageaateetgtetgeateteeaggggagaaggteacaatgaettgeagggeeageteaagtgtaagttaeatgeae
tggtaeeageagaageeaggateeteeeeaaaeeetggatttatgeeeaateetggettetggagteeetgeteegteagt
ggeagtgggtetgggaeetettaeteteteaaateageagagtggaggetgaagatgetgeeaettattaetgeeageagtggagt
tttaaeeeaceeagtteggtgetgggaeeaagetggagetgaagatggeggtggtggtggtggtggatetggagggt
gggageteeaggettatetaeageagttggggetgag (one of the following: ten, aen, gan, ean, aan,

25 **cgn**, **agn**)

gtgaggectggggecteagtgaagatgteetgeaaggettetggetaeaeatttaecagttaeaatatgeaetgggtaaageagaea eetagaeagggeetggaatggattggagetatttateeaggaaatggtgataetteetaeaateagaagtteaagggeaaggeeae aetgaetgtagaeaaateeteeageaeageetaeatgeageteageageetgaeatetgaagaetetgeggtetatttetgtgeaag agtggtgtaetatagtaaetettaetggtaettegatgtetggggeaeagggaeeaggteaeegtetettetgateag

30

Amino acid sequence MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS FNPPTFGAGTKLELKDGGGSGGGGSGGGSGGAYLQQSGAE (one of the following:

35 **S, T, D, E, Q, N, R, K, H)**VRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFK

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GKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVT VSSDQ

2. VHL11 deletion

5 Nucleotide sequence:

Amino acid sequence:

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS 20 FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAEVRPGASVKMSCKA SGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSST AYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQ

3. 2H7 VL L106 with alternative mutations

25 Nucleotide sequence:

Amino acid sequence:

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLE (S, T, R, K, H, Q, N, D, E, and non-natural derivatives of these
amino acids at position 106)KDGGGSGGGGGGGSS

4. VL L106 deletion

40 Nucleotide sequence:

Aagettgeegeeatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgttete teeeagteteeageaateetgetgeateteeagggagaaggteacaatgaettgeagggeeageteaagtgtaagttaeatgeae tggtaceageaggateeteeceaaacetggatttatgeeeeateeaacetggettetggagteetgetteagt ggeagtgggtetgggaeetettaeteteteaaateageagagtggaggetgaagatgetgeeacettataetgeeageagtggagtttaaceeaceaegtteggtgetgggaeeaagetggagagaggtgg

gagete

Amino acid sequence:

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MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS FNPPTFGAGTKLEKDGGGSGGGGSGGGGSS

5 5. **IgE CH3 CH4**

Nucleotide sequence:

Amino acid sequence:

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SNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTR KEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAA PEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRK TKGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK

6. hIgG1H/IgE WCH3 WCH4

Nucleotide sequence:

Amino acid sequence:

35 DQEPKSSDKTHTSPPSPASNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTV NLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHL PRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLH NEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQT VQRAVSVNPGK

7. IgE WCH2 WCH3 WCH4

Nucleotide sequence:

gaggacatcteggtgcagtgcacaacgaggtgcagetcceggacgcccggcacagcacgacgcagcacgcagaaccaagaccaagaccaagacccaagggctccggcttcttcgtcttcagccgcctggaggtgaccagggccgaatgggagcagaaagatgagttcatctgccgtgcagtccatgaggcagcagcagcagcagcagcagcagcagcggtgtctgtaaatcccggtaaatgataatctaga

5 Amino acid sequence:

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DHVCSRDFTPPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDV DLSTASTTQEGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSN PRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKE EKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPE VYAFATPEWPGSRDKRTLACLIONEMPEDISVOWLHNEVOLPDARHSTTOPPKTK

10 VYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTK GSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK

8. hIgG1H/IgE CH3 CH4 (ORF)

Nucleotide sequence:

- 25 Amino acid sequence:
 DQEPKSSDKTHTSPPSPASNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTV
 NLTWSRASGKPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHL
 PRALMRSTTKTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLH
 NEVQLPDARHSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQT
 VQRAVSVNPGKSGSFE

9. 2H7 VHL11S scFv hIgG1(SSS-S)H hIgE WCH3 WCH4

Nucleotide sequence:

- a agett geege cat gg att tte aget ge ag att tte aget te et get aat eagt get te agt cat a att gee ag ag gae aa att get te te te aget geege ag ag gae aa att get et en geege geege ag ag geege ag ag geege g35 cccagtctccagcaatcctgtctgcatctccaggggagaaggtcacaatgacttgcagggccagctcaagtgtaagttacatgcact ggtaccagcagaagccaggatcctcccccaaacctggatttatgccccatccaacctggcttctggagtcctgctcgcttcagtg g cagtgggtctgggacctcttactctctcacaatcagcagagtggaggctgaagatgctgccacttattactgccagcagtggagtttggagcteteaggettatetaeageagtetggggetgagteggtgaggeetggggeeteagtgaagatgteetgeaaggettetgge 40 ggtgataetteetaeaateagaagtteaagggeaaggeeacaetgaetgtagaeaaateeteeageaeageetaeatgeageteag cagcctgacatctgaagactctgcggtctatttctgtgcaagagtggtgtactatagtaactcttactggtacttcgatgtctggggcac agggaccacggtcaccgtctcttctgatcaggagcccaaatcttctgacaaaactcaccatccccaccgtcctcagcatccaacc cgagagggtgagcgcctacctaagccggcccagcccgttcgacctgttcatccgcaagtcgcccacgatcacctgtctggtggt45 ggacetggcacccagcaaggggacegtgaacetgacetggtccegggccagtgggaagcetgtgaaccaetccaccagaaag accagt g cagggt g acceaeccccaect g c caggg c cet cat g c g g t c cae g accaa g accag e g g c c e g c t g c c cae g accaa g acca g e g c c c g c g t g c t g c c c c c a g a c a g a c
- tgaggacatcteggtgeagtgetgeaeaaegaggtgeageteeeggaegeeeggeaeageaegaegeageaegaegeegaagaee
 50 aagggeteeggettettegtetteageegeetggaggtgaceagggeegaatgggageagaaagatgagtteatetgeegtgeag
 teeatgaggeagegageegeteeaagaeegteeagegggtgtetgtaaateeeggtaaatgataatetaga

Amino acid sequence:

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MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
5 FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
THTSPPSSASNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASG
KPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTT
10 KTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDAR
HSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNP
GK

10. 2H7 VHL11S scFv hIgG1(SSS-P)H hIgE WCH3 WCH4

Nucleotide sequence:

a agett g ceg ceat gg at titte a ag t g cag at titte ag ette ctg cta at cag t get teag teat a at t g ceag ag ga caa at t g t ette ctag teat a t t g ceag ag ga caa at t g t t ette ctag t each ctagcccag to to cag caat cot g to tge a to teach gauge gauge gauge gauge to a significant grant grggtaccag caga agce aggate cteece caa accet ggatt tatge coe accet ggettet ggatteet gette gette agt tatget accet gette ggatteet g20 g cagtgggt ctgggacctcttactctctcacaat cag cagatggaggctgaagatgctgccacttattactgccagcagtggagttttaca catttac cagttaca a tatgcact gggtaa ag cag cac cag ga cag gg catt gg a tatttat cag ga a at tatgcact gg a cac tatgcggtgatactteetacaateagaagtteaagggeaaggeeacaetgaetgtagaeaaateeteeageacageetacatgeageteag 25 agggacca eggt caceg to tette t gatcag gag ecca a at ettet gacaa a actea caca acceca ecgt eccea geat ecaa eccae accet eccae eggt excease gatca excea accet eccae eggt excease gatca excegagagggtgagegeetaeetaageeggeeeageeegttegaeetgtteateegeaagtegeeeacgateacetgtetggtggt ggacetggcacccagcaaggggaccgtgaacctgacetggtcccgggccagtgggaagcctgtgaaccactccaccagaaag 30 accagtg cagggtg acceaceccaectg cecaggg cecteatg eggt ceaegaceaa gae cagegg ceceggtg ctg ceceeggaagtetatgegtttgegaegeeggagtggeeggggageegggaeaagegeaecetegeetgeetgateeagaaetteatgee tgaggacateteggtgcagtggctgeacaaegaggtgcageteeeggaegeeeggcaeageaegaegeageeegaagaee a aggget cegget tette g tette ag ceg cet g g aggt g accag g g cega at g g g ag caga a ag at g agtte at et g cegt g caga and g aggt cat et g cegt g caga and g agg et g agg e

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Amino acid sequence:

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK THTSPPSPASNPRGVSAYLSRPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASG KPVNHSTRKEEKQRNGTLTVTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTT KTSGPRAAPEVYAFATPEWPGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDAR HSTTQPRKTKGSGFFVFSRLEVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNP GK

10. 2H7 VL L106S

aagettgeegeeatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgttetet ceeagteteeageaateetgtetgeateteeaggggagaaggteacaatgaettgeagggeeageteaagtgtaagttacatgeaet ggtaceageagaageeaggateeteeeeaaaeeetggatttatgeeeeateeaaeetggettetggagteeetgeteggtteagtg

5 Amino acid sequence:

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MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS FNPTFGAGTKLESKDGGGSGGGGSGGGSS

10 11. 2H7 VL L106S scFv

Nucleotide sequence:

Amino acid sequence:

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY

QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLESKDGGGSGGGGSGGGGSSQAYLQQSGAELVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQ

30 12. 2H7 scFv VL L106S VHL11S scFv

Nucleotide sequence:

Aagettgeegecatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgttete teecagteteeageaateetgtetgeateteeaggggagaaggteaeaatgaettgeagggeeageteaagtgtaagttaeatgeae tggtaecageagaageeaggateeteececaaaceetggatttatgeeceateeaacetggettetggagteeetgeteggteagt

- 40 agcagcetgacatetgaagactetgeggtetatttetgtgeaagagtggtgtaetatagtaactettaetggtaettegatgtetgggge acagggaceaeggteaeegtetettetgateag

Amino acid sequence:

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
45 QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLESKDGGGSGGGGSGGGSSQAYLQQSGAESVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQ

50 10. Human IgD hinge linker with attached restriction sites Nucleotide:

5 Amino acid:

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VDPGSKSPKAQASSVPTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEEQ EERETKTGAVD

Sequence of Native IgD hinge domain:

10 (includes a cysteine residue—we truncated the hinge prior to that residue for these constructs:)

Nucleotide:

Amino acid sequence:

ESPKAQASSVPTAQPQAEGSLAKATTAPATTRNTGRGGEEKKKEKEKEEQEERET KTPECPSHTQPLGVYLLTP

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12. 2H7 VH L11S

Nucleotide sequence:

caggettatetacageagtetgggetgagteggtgaggeetggggeeteagtgaagatgteetgeaaggettetggetacacattt
accagttacaatatgeaetgggtaaageagacacetagacagggeetggaatggattggagetatttatecaggaaatggtgatact
teetacaateagaagtteaagggeaaggeeacactgactgtagacaaatectecagcacagcetacatgcageteagacetga
catetgaagactetgeggtetatttetgtgeaagagtggtgtactatagtaactettactggtacitegatgtetggggeacagggace

aeggteaeegtetettet

Amino acid sequence:

30 QAYLQQSGAESVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPG NGDTSYNQKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYFCARVVYYSNSYWY FDVWGTGTTVTVSS

13. 2H7 VH L11S scFv

35 Nucleotide sequence:

aagettgeegeeatggatttteagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgtteet eeeagteteeageaateetgtetgeateteeaggggagaaggteacaatgaettgeagggeeageteaagtgtaagttacatgeaet ggtaceageagaageeaggateeteeeeaaacetggatttatgeeeeateeaacetggettetggagteetgetgeggaettettaeteteeacaateageagagggaggetgaagatgetgeeacttattaetgeeageagtggagttt

- 45 agggaccacggtcaccgtctcttctgatcag

Amino acid sequence:

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS

50 FNPPTFGAGTKLELKDGGGSGGGGGGGGGGSQAYLQQSGAESVRPGASVKMSCK

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ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQ

14. 2H7 scFv VH L11S hIgG1 (CSC-S)H WCH2 WCH3

5 Nucleotide sequence:

cccagtetecageaateetgtetgeatetecaggggagaaggteacaatgaettgeagggeeageteaagtgtaagttacatgeaet ggtaccagcagaagccaggatcctcccccaaacctggatttatgccccatccaacctggcttctggagtccctgctcgcttcagtg g cagt ggg tot ggg acctet tactet caca at cag cag ag t gg ag ct gaa gat t gc acctet tattact gc cag t ag t gg ag t t t accept the contract of the contract ofggagcteteaggettatetacageagtetggggetgagtetgtgaggeetggggeeteagtgaagatgteetgeaaggettetgget a cac att taccagt taca at at geact gg ta a a geacacct aga cag gg cct gg a at gg at t gg ag ct att taccag ga a at gg at the can geacact ga and ga at gg at the cap ga at gg $\tt ctgggtggaccgtcagtcttcctcttcccccaaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggt$ ggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagc egegggaggagcagtacaacagcaegtacegtgtggtcagegtcetcacegtcetgcaccaggaetggetgaatggcaaggag tacaagtgcaaggtctccaacaaagccctcccagccccategagaaaacaatctccaaagccaaagggcagccccgagaacc a caggig ta caccit g cccccat cccg g at gag ct g acca a gaac caggit cag cct g acct gagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacg geteettetteetetacageaageteaeegtggacaagageaggtggeageaggggaaegtetteteatgeteegtgatgeatgag getetgeacaaccactacacgcagaagagcetetccctgtetccgggtaaatgatetaga

25 Amino acid sequence:

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSCDK
THTSPPCSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE

NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL

35 SPGK

15. 2H7 scFv VH L11S IgE WCH2 WCH3 WCH4

Nucleotide sequence:

40 ${\tt cccag} to {\tt ccag} cate {\tt ctg} to {\tt ctg} cate {\tt ctg} cag {\tt gg} {\tt gag} a {\tt agg} {\tt gtcaca} at {\tt gcag} {\tt gccag} {\tt ctcag} {\tt gtcaca} {\tt gtcaca} {\tt gcag} {\tt gccag} {\tt ctcag} {\tt gtcaca} {\tt gcag} {\tt gccag} {\tt$ ggtaccagcagaagccaggatcctcccccaaacctggatttatgccccatccaacctggcttctggagtcctgctgcttcagtg gcagtgggtctgggacctcttactctcacaatcagcagagtggaggctgaagatgctgccacttattactgccagcagtggagttt ta acceacca c g t t c g g t g c t g g g accea g c t g a g a t g a g g t g g t c g g g t g g t c g g g t g g t c g g g t g g t c g g g t g g t c g g g t g g t c g g g t g gggagctctcaggettatctacagcagtctggggctgagtctgtgaggcctggggcctcagtgaagatgtcctgcaaggcttctggct45 gtgatacticctacaatcagaagttcaagggcaaggccacactgactgtagacaaatcctccagcacagcctacatgcagctcagc agcctgacatctgaagactctgcggtctatttctgtgcaagagtggtgtactatagtaactcttactggtacttcgatgtctggggcaca gggaccacggtcaccgtctcttctgatcacgtctgctccagggacttcaccccgcccaccgtgaagatcttacagtcgtcctgcgac 50 aggacggcaggtcatggacgtggacttgtccaccgcctctaccacgcaggagggtgagctggcctccacacaaagcgagctc accetcagecagaageaetggetgtcagacegeaeetaeaectgeeaggteaectateaaggteaeaectttgaggaeageaeea

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Amino acid sequence:

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MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS FNPPTFGAGTKLELKDGGGSGGGGSGGGGSGGGSSQAYLQQSGAESVRPGASVKMSCK ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDHVCSRDFT PPTVKILQSSCDGGGHFPPTIQLLCLVSGYTPGTINITWLEDGQVMDVDLSTASTTQ EGELASTQSELTLSQKHWLSDRTYTCQVTYQGHTFEDSTKKCADSNPRGVSAYLS RPSPFDLFIRKSPTITCLVVDLAPSKGTVNLTWSRASGKPVNHSTRKEEKQRNGTLT VTSTLPVGTRDWIEGETYQCRVTHPHLPRALMRSTTKTSGPRAAPEVYAFATPEW PGSRDKRTLACLIQNFMPEDISVQWLHNEVQLPDARHSTTQPRKTKGSGFFVFSRL EVTRAEWEQKDEFICRAVHEAASPSQTVQRAVSVNPGK

16. 2H7 scFv VH L11S mIgE WCH2 WCH3 WCH4

25 Nucleotide sequence:

cccagtetecageaateetgtetgeatetecaggggagaaggteaeaatgaettgeagggeeageteaagtgtaagttaeatgeaet ggtaccagcagaagccaggatcctcccccaaaccctggatttatgccccatccaacctggcttctggagtccctgctcgcttcagtg gcagtgggtctgggacctcttactctcacaatcagcagagtggaggctgaagatgctgccacttattactgccagcagtggagttt 30 ta acceacce acgt to gg t g ct gg gacca a g ct g a a g at g g ct g g g t g g t c g g g t g g t c g g g t g g t c g g g t g gggagctctcaggcttatctacagcagtctggggctgagtctgtgaggcctggggcctcagtgaagatgtcctgcaaggcttctggct acacatttaccagttacaatatgcactgggtaaagcagacacctagacagggcctggaatggattggagctatttatccaggaaatg gtgatacttcctaca at caga agttca agggca aggcca cactgactgtaga ca a at cct ccag cacag cct a catgcag ct cagcagect gacatet gaag actet geggtet at the telegrap agagt get gat actet ta agta actet ta et ggt act telegrap ged can be a finished a considerable and the telegrap get gat actet to the telegrap graph of the telegrap graph and the telegrap graph gra35 gggaccacggtcaccgtctcttctgatcacgttcgacctgtcaacatcactgagcccaccttggagctactccattcatcctgcgacc cca at geat to cacteca accate caget gract gette atttat gge cacate cta a at gat gt et et g te aget gget a at gg ac gat can be a considered as a considered at the consideredgggagataactgatacacttgcacaaactgttctaatcaaggaggaaggcaaactagcctctacctgcagtaaactcaacatcactgagcagcaatggatgtctgaaagcaccttcacctgcaaggtcacctcccaaggcgtagactatttggcccacactcggagatgccca 40 ctggtggtggacctggaaagcgagaagaatgtcaatgtgacgtggaaccaagagaagaagacttcagtctcagcatcccagtggt agtgcatagtggaccaccotgattttcccaagcccattgtgcgttccatcaccaagaccccaggccagcgctcagccccgaggta tatgtgttcccaccaccagaggaggagagcgaggacaaacgcacactcacctgtttgatccagaacttcttccctgaggatatctct 45 ggettetteatetteagtegeetagaggtegeeaagaeaetetggaeaeagagaaaaeagtteaeetgeeaagtgateeatgagge actteaguaacceaggaaactggagaaaacaatateeacaagcettggtaacaceteecteegteeateetagtaatetagag

Amino acid sequence:

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
50 QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGSSQAYLQQSGAESVRPGASVKMSCK

ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDHVRPVNIT EPTLELLHSSCDPNAFHSTIQLYCFIYGHILNDVSVSWLMDDREITDTLAQTVLIKE EGKLASTCSKLNITEQQWMSESTFTCKVTSQGVDYLAHTRRCPDHEPRGVITYLIP PSPLDLYQNGAPKLTCLVVDLESEKNVNVTWNQEKKTSVSASQWYTKHHNNATT SITSILPVVAKDWIEGYGYQCIVDHPDFPKPIVRSITKTPGQRSAPEVYVFPPPEEESE DKRTLTCLIQNFFPEDISVQWLGDGKLISNSQHSTTTPLKSNGSNQGFFIFSRLEVAK TLWTQRKQFTCQVIHEALQKPRKLEKTISTSLGNTSLRPS

10 17. 2H7 scFv VH L11S hIgA WH WCH2 T4CH3

Nucleotide sequence:

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30 gaggtggactgataatctaga

Amino acid sequence:

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCOOWS

- 35 FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQPVPSTPPT PSPSTPPTPSPSCCHPRLSLHRPALEDLLLGSEAILTCTLTGLRDASGVTFTWTPSSG KSAVQGPPDRDLCGCYSVSSVLPGCAEPWNHGKTFTCTAAYPESKTPLTATLSKS
- 40 GNTFRPEVHLLPPPSEELALNELVTLTCLARGFSPKDVLVRWLQGSQELPREKYLT WASRQEPSQGTTTFAVTSILRVAAEDWKKGDTFSCMVGHEALPLAFTQKTIDRLA GKPTHVNVSVVMAEVD

18. 2H7 scFv VH L11S mIgA WH WCH2 T4 CH3

45 Nucleotide sequence:

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Amino acid sequence:

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15 MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDHICSPPTTP
20 PPPSCQPSLSLQRPALEDLLLGSDASITCTLNGLRDPEGAVFTWEPSTGKDAVQKK
AVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDTLTGTIAKVTVNTFPPQV
HLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYLVFEPLKEPGE
GATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRLSGKPTNVSVS
VIMSEGD

A. mIgA WCH2 T4CH3

Nucleotide sequence:

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Amino acid sequence:

DHICSPPTTPPPPSCQPSLSLQRPALEDLLLGSDASITCTLNGLRDPEGAVFTWEPST

GKDAVQKKAVQNSCGCYSVSSVLPGCAERWNSGASFKCTVTHPESDTLTGTIAKV

TVNTFPPQVHLLPPPSEELALNELVSLTCLVRAFNPKEVLVRWLHGNEELSPESYL

VFEPLKEPGEGATTYLVTSVLRVSAEIWKQGDQYSCMVGHEALPMNFTQKTIDRL

SGKPTNVSVSVIMSEGD

45 20. K322S CH2 region

Nucleotide sequence:

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Amino acid sequence:

PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCSVSNKALPAPIEKTISKAK

21. K322S CH2 WCH3

Nucleotide sequence:

cetgaacteetggggggacegteagtetteetetteeceecaaaaceeaaggacaceeteatgateteeeggaceetgaggteae
atgegtggtggtggacgtgagccacgaagaceetgaggteaagtteaactggtacgtggacggegtggaggtgcataatgeeaa
gacaaageegegggaggagcagtacaacagcacgtacegtgtggteagegteeteacegteetgcaceaggactggetgaatg
gcaaggagtacaagtgeteggteteeaacaaageeeteecageeeecategagaaaacaateteeaaageeaaagggeageee
egagaaceacaggtgtacaceetgeeeecateeegggatgagetgaceaaggacaacaggteageetggteaaagg
ettetateecagegacategeegtggagtgggagagcaatgggeageeggagaacaactacaagaceacgeeteeegtgg
acteegacggeteettetteetetacagcaagetcacegtggacaagaggggaacgtetteteatgeteegtg
atgeatgaggetetgeacaaccactacacgcagaagaggceteteeegggtaaatgatetaga

Amino acid sequence:

PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCSVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

1. K322L CH2 WCH3

Nucleotide sequence:

tgatcaggagcccaaatcttctgacaaaactcacacatccccaccgtcctcagcacctgaactcctggggggaccgtcagtcttcct
 otteccccaaaacccaaggacacctcatgatctcccggaccctgaggtcacatgcgtggtggtggacgtgagccacgaaga
 ccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcgggaggagcagtacaaca
 gcacgtaccgtgtggtcagcgtcctcaccgtcctgaccaggactggctgaatggcaaggagtacaaagtgcctggtctccaacaa
 agccctcccagcccccatcgagaaaacaatctccaaagccaaaggcagccccgagaaaccacaggtgtacacctgccccat
 cccgggatgagctgaccaagaaccacggtcagctgactgctgactgctgacaaggcttctatcccagcgacatcgccgtggagtggg
 agagcaatgggcagccggagaaacaactacaagaccacgcctcccgtgctgactcgactgcagggcacccttcttctcctctacagcaagct
 caccgtggacaagagcaggtgcagcaggggaacgtcttctatgctcgtgatgcatgaggctctgacaaaccactacacgca
 gaagagcctctccctgtctccgggtaaatgatctaga

35 Amino acid sequence:

40

DQEPKSSDKTHTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHED PEVKFNWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCLV SNKALPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVE WESNGQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHN HYTQKSLSLSPGK

22. 2H7 scFv VHL11S hIgG1 (SSS-S)H K322SCH2 WCH3 Nucleotide sequence:

Amino acid sequence:

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MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
THTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCSVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

23. 2H7 scFv VHL11S hIgG1 (SSS-S)H K322LCH2 WCH3

Nucleotide sequence:

a agett g cegecatgg at ttt caagt g cag at ttt cagett cet get a at cag t get teagt cat a at t g ceag agg a caa at t g t cet teagt can be a supported by the company of theggtaccag cag a agc cag gat cet cecccaa accet gg at that generate caacet gg etter gg agt ceet get cag the same partial of the same partial content of the same partial cogcagtgggtctgggacctcttactctcacaatcagcagagtggaggctgaagatgctgccacttattactgccagcagtggagttt ggagctctcaggcttatctacagcagtctggggctgagtcggtgaggcctggggcctcagtgaagatgtcctgcaaggcttctggctacacatttaccagttacaatatgcactgggtaaagcagacacctagacagggcctggaatggattggagctatttatccaggaaatggtgata ctt ccta ca a t caga a g t ca a gg c ca cact ga ct gt a ga ca a a t cct c cag ca ca g c t ca g caca t cat g ca g ct a cat g ca g ct ca g caca t cat g ca g ct ca g caca t cat g ca g ct ca g caca t cat g caca t cacaagggaccacggtcaccgtctcttctgatcaggagcccaaatcttctgacaaaactcacacatccccaccgtcctcagcacctgaactcctggggggaccgtcagtcttcctcttcccccaaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggcgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagta ca agt geot g g to te caa caa ag e ce te ce ag e ce ce a te gagaa a acaa to te caa ag e caa ag g g cag e ce c g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e caa ag g g cag e ce g ag aa ce a caa ag e ccaggtgtacaccetgcccccatecegggatgagetgaceaagaaccaggtcageetgacetgeetggtcaaaggettetatecea gcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacggctctg caca accacta cacg caga agag cctctccctg tctccg gg taa at gat ctaga

Amino acid sequence:

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK

THTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCLVSNKALPAPIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS PGK

24. 2H7 scFv VHL11S hIgG1 (CSS-S)H K322SCH2 WCH3

Nucleotide sequence:

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a agett geogecatgg at ttt caa gt georga at ttt cagett cet get a at cagt get te agt cata at t georga gag acaa at t gt te te to the same at the same a10 ggtaccag cag a age cag gate ctcccccaaa acctg gatt tat ge ce caacet gget tet gg agt ecct get cag tat gate can be considered as a considered considered and considered age to consider a considered age to considered age to consider a considered age to cggageteteaggettatetacageagtetggggetgagteggtgaggeetggggeeteagtgaagatgteetgeaaggettetggeaggetgaggeeteagtgaggeeta cacattta ccagtta caatat gcact gggtaa ag cacacatag a cag ggcct ggaat ggatt ggag ctattta tccag gaa at the companion of the15 agggaccacggtcaccgtctcttctgatcaggagcccaaatcttgtgacaaaactcacacatccccaccgtcctcagcacctgaact cctggggggaccgtcagtcttcctcttcccccaaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtgg 20 cgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgagg25 etct geaca accaeta cae geaga agage ctet ceet glet ceg ggtaa at gateta ga

Amino acid sequence:

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGSGGGSSQAYLQQSGAESVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSCDK
THTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCSVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

40 25. P331S CH2

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Nucleotide sequence:

cetgaacteetggggggacegteagtetteetetteececcaaaacceaaggacaceteatgateteeggaceetgaggteacatgegtggtggtggaegtgagceacgaagaceetgaggteaagtteaactggtaegtggaeggegtggaggtgeataatgeeaa gacaaagcegegggaggagcagtacaacagcacgtaeegtggteagegteeteacegteetgeaceaggaetgaatg geaaggagtacaagtgeaaggteteeaacaaagceeteecageeteeategagaaaaacaateteeaaagceaaa

Amino acid sequence PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAK

26. P331S CH2 WCH3

http://www.patentions.net/

WO 2005/017148 PCT/US2003/041600

Nucleotide sequence:

 $\verb|cctgaactcctggggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcac||$ atgcgtggtggacgtgaacgtgaacgcacgaagaccctgaagtcaacttgatacgtggacggcgtggaaggtgcataatgccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatg ettetateceagegacategeegtgggagtgggaggcaatgggcageeggagaacaactacaagaccaegeeteeegtgetgg acteegaeggeteettetteetetaeageaageteaeegtggaeaagageaggtggeageaggggaaegtetteteatgeteegtg atgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

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Amino acid sequence

PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGOPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

27. 2H7 scFv VH L11S (SSS-S)H P331S CH2 WCH3

Nucleotide sequence:

 $a agett g {\tt ccgccatggattttcaagtgcagattttcagettcctgctaatcagtgcttcagtcataattgccagaggacaaattgttctct}$ 20 cccagtctccagcaatcctgtctgcatctccaggggagaaggtcacaatgacttgcagggccagctcaagtgtaagttacatgcact ggtaccagcagaagccaggatcctcccccaaaccctggatttatgccccatccaacctggcttctggagtccctgctcgcttcagtg g cagtgggtctgggacctcttactctctcacaatcagcagagtggaggctgaagatgctgcacttattactgccagcagtggagtttta acceacce acg ttcgg tgctgggacca agctggagctgaa agatggcggtggctcgggcggtggtggatctggaggaggtgggageteteaggettatetaeageagtetggggetgagteggtgaggeetgggggeeteagtgaagatgteetgeaaggettetgge 25 tacacatttaccagttacaatatgcactgggtaaagcagacacctagacagggcctggaatggattggagctatttatccaggaaat agggaccacggtcaccgtctcttctgatcaggagcccaaatcttctgacaaaactcacacactccccaccgtcctcagcacctgaactcctggggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtgg 30 tggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggggtggaggtgcataatgccaagacaaagc cgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctccagcctccatcgagaaaacaatctccaaagccaaagggcagccccgagaacca gcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacgg 35 ctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

Amino acid sequence

- MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY 40 QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS FNPPTFGAGTKLELKDGGGSGGGGSGGGSSQAYLQQSGAESVRPGASVKMSCK ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK THTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV 45 DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
- NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS PGK

Nucleotide sequence:

aagettgeegeeatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgttetet cccagtetecageaateetgtetgeatetecaggggagaaggteacaatgaettgeagggeeageteaagtgtaagttacatgeaet ggtaccag caga agc cagga tectecccaa accet gg at that generate caacet gg etter gg agt ceet get teget the grant of the second control of the second controlgcagtgggtctgggacctcttactctctcacaatcagcagagtggaggctgaagatgctgccacttattactgccagcagtggagttt taacccaccacgttcggtgctgggaccaagctggagctgaaagatggcggtggctcgggcggtggtggtctggaggaggtg ggagctctcaggcttatctacagcagtctggggctgagtcggtgaggcctgggggcctcagtgaagatgtcctgcaaggcttctggc10 cagcet gacatet gaag actet geggtet att tet gt geaag ag t g statet at a gt aactet ta et get act te g gt act tet g g g g eacte gat get et g g g g eacte g act tet g g g g eacte g act tet g g g g eacte g act tet g g g g eacte g eacte g act tet g g g g eacte g eacteagggaccacggtcaccgtctcttctgatcaggagcccaaatcttgtgacaaaactcacacatccccaccgtcctcagcacctgaactcctggggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtgg tggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagc cgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggag 15 ta caagt g caag g to to caa caa a g coctoc cag cot coat c g agaa aa caat o to caa a g coa a a g g caa a g caa a g g caa a g g caa a g g caa a g caa a g caa a g g caa a g g caa a g g caa a g caa a g g caa a g caacaggtgtacaccetgccccatcccgggatgagetgaccaagaaccaggtcagcetgacetgctgtcaaaggettetatccca gcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtggtggactccgacgg eteettetteetetaeageaageteaeegtggaeaagageaggtggeageaggggaaegtetteteatgeteegtgatgeatgagg ctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

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Amino acid sequence

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK
25 ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSCDK
THTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPASIE
KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN

NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS

PGK

29. **T256N CH2 region**

Nucleotide sequence:

Cctgaactcctggggggaccgtcagtcttcctcttcccccaaaacccaaggacacctcatgatctcccggaaccctgaggtca catgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgcca agacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaat ggcaaggagtacaagtgcaaggtctccaacaaagccctcccagccccatcgagaaaacaatctccaaagccaaa

40 Amino acid sequence

 $\label{lem:pellggpsvflfppkpkdtlmisrnpevtcvvdvshedpevkfnwyvdgvevhn \\ AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK$

30. **T256N CH2 WCH3**

45 Nucleotide sequence:

actecgaeggeteettetteetetaeageaageteaeegtggaeaagaggtggeageaggggaaegtetteteatgeteegtg atgeatgaggetetgeaeaaceaetaeaegeagaagageeteteeetgteteegggtaaatgatetaga

Amino acid sequence

http://www.patentions.net/

5 PELLGGPSVFLFPPKPKDTLMISRNPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

10 31. 2H7 scFv VH L11S (SSS-S)H T256N CH2 WCH3

Nucleotide sequence:

aagettgeegeeatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgttetet cccag tete cag caate ct g tet g cate te cag g g g ag a a g g tea caat g act t g cag g g c cag et caa g t g ta g tea cat g cae t g cag g g cag g tea cag g g cag g tea cag g g cag g cag15 ggtaccagcagaagccaggatcctcccccaaaccctggatttatgccccatccaacctggcttctggagtccctgctcgcttcagtg g cagtgggtctgggacctcttactctctcacaatcagcagagtggaggctgaagatgctgccacttattactgccagcagtggagttttaacccaccacgttcggtgctgggaccaagctggagctgaaagatggcggtggctcgggcggtggtggtctggaggaggtg ggagctctcaggcttatctacagcagtctggggctgagtcggtgaggcctggggcctcagtgaagatgtcctgcaaggcttctggc 20 cagcctgacatctgaagactctgcggtctatttctgtgcaagagtggtgtactatagtaactcttactggtacttcgatgtctggggcac ectggggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccggaaccctgaggtcacatgcgtgg tggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagc 25 egegggaggagcagtacaacagcacgtaccgtgtggtcagcgtcetcaccgtcetgcaccaggactggetgaatggcaaggag tacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaacaatctccaaagccaaagggcagccccgagaacc agcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacg geteettetteetetacageaageteacegtggacaagageaggtggeageaggggaaegtetteteatgeteegtgatgeätgag 30 gctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

Amino acid sequence

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
THTSPPSSAPELLGGPSVFLFPPKPKDTLMISRNPEVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI
EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

32. 2H7 scFv VH L11S (CSS-S)H T256N CH2 WCH3

Nucleotide sequence:

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aagettgeegecatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggacaaattgtteet ceeagteteeageaateetgtetgeateteeagggagaaaggteacaatgaettgeagggeeageteaagtgaagttacatgeaet ggtaceageagaageeagateeteeeeaaaceetggatttatgeeeeateeaacetggettetggagteetggagteetgegteagtggagtttatgeeeateeagagggggtgaagatgetgeeagttggagtttatateetgeeagagggggtgaagatggaggtgaagatgetgeeagttggagttttaaceeaceacgtteggtgetgggaceaagetggagetgaaagatggeggtggtggtggtggatetggaggaggtg

tacac atttac cagttac aatatg cactgggtaa ag cag acacctag acag ggcctgga at ggattggag ctatttat ccag gaa at the cagtac acctaga cag ggcctgga at the cag gaa acctaga cag gaa aagggaccacggtcaccgtctcttctgatcaggagcccaaatcttgtgacaaaactcacacatccccaccgtcctcagcacctgaactcctggggggaccgtcagtcttcctcttcccccaaaaacccaaggacaccctcatgatctcccggaaccctgaggtcacatgcgtggcgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagccccatcgagaaaacaatctccaaagccaaagggcagcccgagaacc 10 age gacatege c g t g g ag t g g g ag ag caat g g g cag c g g ag aa caacta caa g accae g cet c c g t g c t g g act c c g ac g accae g cat g catgetetgeacaaccactacacgcagaagagcetetecetgteteegggtaaatgatetaga

- 15 Amino acid sequence MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS FNPPTFGAGTKLELKDGGGSGGGGGGGGSSQAYLQQSGAESVRPGASVKMSCKASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
- TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSCDK20 THTSPPSSAPELLGGPSVFLFPPKPKDTLMISRNPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL 25 SPGK*

RTPE/QNAK (255-258) CH2 33.

Nucleotide sequence:

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30 gacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaacaaagccctcccagccccatcgagaaaacaatctccaaagccaaa

Amino acid sequence

 ${\tt PELLGGPSVFLFPPKPKDTLMISQNAKVTCVVVDVSHEDPEVKFNWYVDGVEVHN}$ 35 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK

RTPE/QNAK (255-258)CH2 WCH3 34.

Nucleotide sequence:

- cct gaact cct ggggggaccgt cag tct tcct ctt cccccaaaaacccaa ggacaccct cat gat ctccca gaac gct aa ggt cacgacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggetgaatg gcaaggagtacaagtgcaaggtctccaacaaagccctcccagcccccatcgagaaaacaatctccaaagccaaagggcagccc cgagaacca caggtgta caccet gecce catce cgggatgaget gacca agaaccaggt cage ct gacct gect ggt caa agg45
- act ccg acgget cct tct tcct ctacag caa gct caccgt gg acaa gag caggt gg cag caggg gaa cgt ctt ctcat gct ccgt gag acgget gg cag caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gaa cgt ctt ctcat gct ccgt gag acgget gg caggg gag acgget gg caggg gag acgg gag acgat geat gagget et geaca accaeta cae geaga agage et et ceet get et ce ggg ta a at gate taga

Amino acid sequence

PELLGGPSVFLFPPKPKDTLMISQNAKVTCVVVDVSHEDPEVKFNWYVDGVEVHN 50 AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG

QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

35. 2H7 scFv VH L11S (SSS-S)H RTPE/QNAK (255-258)CH2 WCH3

Nucleotide sequence:

aagettgeegeeatggattiteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgttetet cccag tete cag caat cet g tet g cate te cag g g g ag a a g g tea caat g a ct t g cag g g c cag et caa g t g taa g t t a cat g caet g cag g g cag et caa g t g t a cat g caet g cae g c cag et caa g t g t a cat g caet g cae g caeggtaccag cag a agc cag gat cet cece caa accet gg at that ge cecate caacet gg etter gg agt cect get eget the gat the same parameters of the contract of the contract grant grgcagtgggtctgggacctcttactctcacaatcagcagagtggaggctgaagatgctgccacttattactgccagcagtggagttt taacccaccacgttcggtgctgggaccaagctggagctgaaagatggcggtggctcgggcggtggtggtggatctggaggaggtg ggagetete aggettate tacage agtet gggget gagteggt gagge et ggggeet eagt gaag at gte et geaggettet ggggeet tagget gagget tagge ggggeet gagteggt gagget gagget et gggggeet gagteggt gagget gaggt gagget gaggt gaggt gagget gagget gagget gagget gagget gaggt gagget gagget gagget gagget gagget gataca catttac cag ttaca at at geact gg taa ag cag acacctag a cag gg cet gg a at gg at t gg ag ctatttat ceag ga a at the cag ga acacctag acag gg cet gg and gg at the cag ga acacctag acag gg cet gg and gg at the cag ga acacctag acag gg cet gg and gg at the cag ga acacctag acag gg cet gg and gg at the cag ga acacctag acad gg acacctag acad gg at the cag ga acacctag acad gg at the cag ga acacctag acad gg acacctag acad gg at the cag ga acacctag acad gg accagcctgacatctgaagactctgcggtctatttctgtgcaagagtggtgtactatagtaactcttactggtacttcgatgtctggggcac agggaccacggtcaccgtctcttctgatcaggagcccaaatcttctgacaaaactcacacatccccaccgtcctcagcacctgaactcctggggggaccgtcagtcttcctcttcccccaaaaacccaaggacaccctcatgatctcccagaacgctaaggtcacatgcgtggtggtggacgtgagccacgaagaccotgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagc cgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggag agcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacy geteettetteetetacageaageteaeegtggacaagageaggtggcageaggggaaegtetteteatgeteegtgatgeatgag getetgeacaaccactacaegeagaagageeteteeetgteteegggtaaatgatetaga

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Amino acid sequence
MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
THTSPPSSAPELLGGPSVFLFPPKPKDTLMISQNAKVTCVVVDVSHEDPEVKFNWY
VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI

EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE
35 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL
SPGK

36. 2H7 scFv VH L11S (CSS-S)H RTPE/QNAK (255-258)CH2 WCH3 Nucleotide sequence:

Amino acid sequence

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MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSCDK
THTSPPSSAPELLGGPSVFLFPPKPKDTLMISQNAKVTCVVVDVSHEDPEVKFNWY

15 VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK

20 36. **K290Q CH2 region**

Nucleotide sequence:

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Amino acid sequence:

PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTQPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK

37. K290Q CH2 WCH3

Nucleotide sequence:

Amino acid sequence:

PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTQPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKG QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

38. 2H7 scFv VH L11S (SSS-S)H K290Q CH2 WCH3

Nucleotide sequence:

50 aagettgeegeeatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggacaaattgttetet eceagteteeageaateetgetgeateteeaggggagaaggteacaatgaettgeagggeeageteaagtgtaagttacatgeaet

ggtaccagcagaagccaggatcctcccccaaaccctggatttatgccccatccaacctggcttctggagtccctgctcgcttcagtg geagtgggtetgggacetettaeteteacaateageagagtggaggetgaagatgetgecaettattaetgecageagtggagttt taacceaccacgttcggtgctgggaccaagctggagctgaaagatggcggtggctcgggcggtggtggtctggaggaggtg ggageteteaggettatetaeageagtetggggetgagteggtgaggeetggggeeteagtgaagatgteetgeaaggettetgge tacacatttaccagttacaatatgcactgggtaaagcagacacctagacagggcctggaatggattggagctatttatccaggaaat ggtgatacttcctaca at caga agttca aggcca aggcca cactgactgtaga caaatcctccagca cagcctacatgcagctcagcagcctgacatctgaagactctgcggtctatttctgtgcaagagtggtgtactatagtaactcttactggtacttcgatgtctggggcac agggaccacggtcaccgtctcttctgatcaggagcccaaatcttctgacaaaactcacacactccccaccgtcctcagcacctgaact cctggggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtgg 10 tggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacacagc cgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggag tacaagtgcaaggtetecaacaaageceteccagececcategagaaaacaatetecaaagecaaagggcageeegagaace 15 geteettetteetetacageaageteacegtggacaagageaggtggcageaggggaaegtetteteatgeteegtgatgcatgag gctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

Amino acid sequence:

http://www.patentions.net/

- MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
 QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
 FNPPTFGAGTKLELKDGGGSGGGGSGGGSSQAYLQQSGAESVRPGASVKMSCK
 ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
 TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
 THTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
 DGVEVHNAKTQPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
 KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
 NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
 PGK
- 30 39. 2H7 scfv VH L11S (CSS-S)H K290Q CH2 WCH3

Nucleotide sequence:

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aagcttgccgccatggattttcaagtgcagattttcagcttcctgctaatcagtgcttcagtcataattgccagaggacaaattgttctct cccagtetecageaateetgtetgeatetecaggggagaaggteacaatgaettgeagggeeageteaagtgtaagttaeatgeaet ggtaccag caga age cagga tecteccccaa accet gg at that generate caacet gg etter gg agt ceet get caget to get the sum of tgcagtgggtctgggacctcttactctctcacaatcagcagagtggaggctgaagatgctgccacttattactgccagcagtggagttt taacccaccacgttcggtgctgggaccaagctggagctgaaagatggcggtggctcgggcggtggtggatctggaggaggtg ggagetete aggettate tacage agtet gggget gagteggt gaggeet tggggeet cagt gaag at gteet geaagget tet ggetacacatttaccagttacaatatgcactgggtaaagcagacacctagacagggcctggaatggattggagctatttatccaggaaat ggtgatacttectaeaateagaagtteaagggeaaggeeacactgactgtagacaaatecteeageacageetacatgeageteag cagcctgacatctgaagactctgcggtctatttctgtgcaagagtggtgtactatagtaactcttactggtacttcgatgtctggggcac agggaccacggtcaccgtctcttctgatcaggagcccaaatcttgtgacaaaactcacacatccccaccgtcctcagcacctgaactcctggggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtgg tggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacacagc tacaagtgcaaggtctccaacaaagccctcccagccccategagaaaacaatctccaaagccaaagggcagccccgagaacc agogacatogcogtggagtgggagagcaatgggcagcoggagaacaactacaagaccacgcotocogtgctggactocgacg gctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

Amino acid sequence:

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS FNPPTFGAGTKLELKDGGGSGGGGSGGGGSGGGSSQAYLQQSGAESVRPGASVKMSCK ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSCDK THTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV DGVEVHNAKTQPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS PGK

40. A339PCH2

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Nucleotide sequence:

cetgaacteetggggggacegteagtetteetetteececcaaaacccaaggacacecteatgateteeeggacecetgaggteae
atgegtggtggtggaegtgagecaegaagaceetgaggteaagtteaactggtaegtggaeggtggaggtgeataatgeeaa
gacaaageegegggaggageagtacaaeageaegtaeegtgtggteagegteeteaeegteetgeaeeagaetggetgaatg
geaaggagtaeaagtgeaaggteteeaaeaaageeeteeeageeeecaaegaaaaacaateteeaaaeeeaaa

Amino acid sequence:

20 PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKPK

41. A339P CH2 WCH3

25 Nucleotide sequence:

35 Amino acid sequence:

PELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHN AKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKPKG QPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV LDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

42. 2H7 scFv VHL11S (SSS-S)H A339P CH2 WCH3

Nucleotide sequence:

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Amino acid sequence:

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK
15 ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
THTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKPKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

43. 2H7 scFv VHL11S (CSS-S)H A339P CH2 WCH3

25 Nucleotide sequence:

a agett geegee at ggattite aget geag at titte agetteet get aat eagt gette aget at at tigee ag aggae aa at tigteet en tigee geegee aget gette aget gette aget gette ag tigee geegee ag aggae ag at titte aget gette gette ag tigee geegee gette gette ag tigee geegee gette gette ag tigee gette gettcccag to tecage a at cet get each extraction and the constraint of the constraintggtaccag cag gaag ccag gate ctcccccaa accet ggatt tat geec cate caacet gget tet ggag te cet get cag tat gate can be a considered and the considered considered accet grant and the considered considered considered accet grant and the considered considered considered accet grant and the considered consideredg cag t g g g acctetta ctete teaca at cag cag a g t g g a g c t g a a g at g c t g cae t t at ta e t g c cae t t at t a cae t at ta e t g c cae t t at t a cae t at t a cae t at t a cae t a cae t at t a cae t a cae30 ggageteteaggettatetaeageagtetggggetgagteggtgaggeetgggggeeteagtgaagatgteetgeaaggettetgge ta ca cattta ccagtta caatat gcactgggtaa ag cag ac acctag a cag ggcctggaat ggattggag ctattta tccag gaa at account of the compact of the compact account of thecagcet gacatet gaag actet geggtet att tet gtg caag ag t g tactat ag taactet tact g g tact te gat g tet g g g caeagggaccacggtcaccgtctcttctgatcaggagcccaaatcttgtgacaaaactcacacatccccaccgtcctcagcacctgaact35 cctggggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggta ca agt g ca ag g to to ca aca a ag coctoc ca g ca coc catega ga a a aca at ctoca a accea ag g g ca g coc e g ag a accea ag a coc e g ag a accea ag g a accea ag a g a accea ag a coc e g ag a accea ag a coc e g ag a accea ag a coc e g a accea accea ag a coc e g a accea accea ag a coc e g a accea accea ag a coc e g a accea accea accea accea ag a coc e g a accea aca caggitg tacaccet g cocccate cogggatg agetg accaaga accaggit cage ctg acct g cot g g to a agget the tate comparison of the contract of the40 agcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacg gctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

45 Amino acid sequence:

50

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSCDK THTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV

DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE KTISKPKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS PGK

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44. G28-1VH

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Nucleotide sequence:

geggtecagetgeageagtetggacetgagetggaaaageetggegetteagtgaagattteetgeaaggettetggttacteatte
actggetacaatatgaactgggtgaageagaataatggaaagacettgagtggattggaaatattgateettattatggtggtaeta
ectacaaceggaagtteaagggeaaggeeacattgactgtagacaaateeteeageacageetacatgeageteaaggtetgae
atetgaggactetgeagtetattactgtgeaagateggteggeeetatggactactggggteaaggaaceteagteacegtetettet
gateag

15 Amino acid sequence:

AVQLQQSGPELEKPGASVKISCKASGYSFTGYNMNWVKQNNGKSLEWIGNIDPY YGGTTYNRKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVYYCARSVGPMDYWG QGTSVTVSSDQ

20 45. G28-1VL

Nucleotide sequence:

aagettgeegeeatggtateeaeageteagtteettgggttgetgetgetgtggettaeaggtggeagatgtgacateeagatgacte agteteeageeteectatetgeatetgtgggagagactgteaceateacatgtegaacaagtgaaaatgtttaeagttatttggettggt ateageagaaaaaagggaaaaateteeteageteetggtetettttgeaaaaaacettageagaaggtgtgeeateaaggtteagtggea gtggateaggeacaaagttttetetgaagateageageetgeageetgaagattetggaagttatttetgteaacateatteegataat eegtggaegtteggtggaggeacegaactggagateaaaggtggeggtggetegggeggtggtgggtegggtggegggateeg

Amino acid sequence:

30 MVSTAQFLGLLLWLTGGRCDIQMTQSPASLSASVGETVTITCRTSENVYSYLAW YQQKQGKSPQLLVSFAKTLAEGVPSRFSGSGSGTQFSLKISSLQPEDSGSYFCQHHS DNPWTFGGGTELEIKGGGGSGGGGSGGGSS

35 46. G28-1 scFv

Nucleotide sequence:

Amino acid sequence:

MVSTAQFLGLLLWLTGGRCDIQMTQSPASLSASVGETVTITCRTSENVYSYLAW YQKQGKSPQLLVSFAKTLAEGVPSRFSGSGSGTQFSLKISSLQPEDSGSYFCQHHS DNPWTFGGGTELEIKGGGGSGGGGSGGGGSSAVQLQQSGPELEKPGASVKISCKA 10

- 25

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 $SGYSFTGYNMNWVKQNNGKSLEWIGNIDPYYGGTTYNRKFKGKATLTVDKSSST\\ AYMQLKSLTSEDSAVYYCARSVGPMDYWGQGTSVTVSSDQ$

5 47. **G28-1 VHL11S**

Nucleotide sequence:

gcggtccagctgcagcagtctggacctgagtcggaaaagcctggcgcttcagtgaagatttcctgcaaggcttctggttactcattc actggctacaatatgaactgggtgaagcagaataatggaaagagccttgagtggattggaaatattgatccttattatggtggtacta cctacaaccggaagttcaagggcaaggccacattgactgtagacaaatcctccagcacagcctacatgcagctcaagagtctgac atctgaggactctgcagtctattactgtgcaagatcggccctatggactactggggtcaaggaacctcagtcaccgtctcttct gatcag

Amino acid sequence:

15 AVQLQQSGPESEKPGASVKISCKASGYSFTGYNMNWVKQNNGKSLEWIGNIDPYY GGTTYNRKFKGKATLTVDKSSSTAYMQLKSLTSEDSAVYYCARSVGPMDYWGQ GTSVTVSSDQ

20 48. G28-1 VHL11S scFv

Nucleotide sequence:

Amino acid sequence:

ttctgatcag

MVSTAQFLGLLLLWLTGGRCDIQMTQSPASLSASVGETVTITCRTSENVYSYLAW
YQQKQGKSPQLLVSFAKTLAEGVPSRFSGSGSGTQFSLKISSLQPEDSGSYFCQHHS
DNPWTFGGGTELEIKGGGGSGGGGSGGGSSAVQLQQSGPESEKPGASVKISCKA
SGYSFTGYNMNWVKQNNGKSLEWIGNIDPYYGGTTYNRKFKGKATLTVDKSSST
AYMQLKSLTSEDSAVYYCARSVGPMDYWGQGTSVTVSSDQ

40 49. G28-1 scFv (SSS-S)H WCH2 WCH3

Nucleotide sequence:

10 Amino acid sequence:

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MVSTAQFLGLLLWLTGGRCDIQMTQSPASLSASVGETVTITCRTSENVYSYLAW YQQKQGKSPQLLVSFAKTLAEGVPSRFSGSGSGTQFSLKISSLQPEDSGSYFCQHHS DNPWTFGGGTELEIKGGGGSGGGGSGGGGSSAVQLQQSGPELEKPGASVKISCKA SGYSFTGYNMNWVKQNNGKSLEWIGNIDPYYGGTTYNRKFKGKATLTVDKSSST

15 AYMQLKSLTSEDSAVYYCARSVGPMDYWGQGTSVTVSSDHDQEPKSSDKTHTSP PSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

50. G28-1 scFv IgAW H IgG1WCH2 WCH3

Nucleotide sequence:

a agett geogecatg glate cacage teagtt cett gg gtt get get gg gett acag gt gg cag at gt gacate cag at gacte get gg get gacat gacage gat gacate gacage gacagagtete cage et cectatet geat et gegagagaga et geae cateacat gegaaca agt gaa a at gitt a cag that the getter general general25 gtggatcaggeacacagttttctctgaagatcagcagcctgaagattctggaagttatttctgtcaacatcattccgataatus to the second state of the second stateactacctaca accgga a gttca agggca aggcca cattgactgtaga caa atcctccag cacagcctacatgcagctca agagtctacatgcagctca aggreent aggreent according to the contract of the contract of30 ttetgateageeagtteecteaacteeacetaceecateteecteaacteeacetaceecateteecteatgegeacetgaacteetggggggaccgt cag tette ctette cece caa aacce aaggacae cete at gate te ceg gacce ct gag gt cae at geg t gg t gg te gag gacce ct gag gacce gacce gag gacce gacce gag gacce gacce gacce gag gacce ggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagccgcg35 gtgcaaggtctccaacaaagccctcccagcccccatcgagaaaacaatctccaaaggccaaagggcagccccgagaaccacagg categoegtggagtgggagagcaatgggcagceggagaacaactacaagaccaegcetccegtgetggacteegacggetcet40 cacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

Amino acid sequence:

MVSTAQFLGLLLLWLTGGRCDIQMTQSPASLSASVGETVTITCRTSENVYSYLAW
YQQKQGKSPQLLVSFAKTLAEGVPSRFSGSGSGTQFSLKISSLQPEDSGSYFCQHHS
DNPWTFGGGTELEIKGGGGSGGGGSGGGSSAVQLQQSGPELEKPGASVKISCKA
SGYSFTGYNMNWVKQNNGKSLEWIGNIDPYYGGTTYNRKFKGKATLTVDKSSST
AYMQLKSLTSEDSAVYYCARSVGPMDYWGQGTSVTVSSDQPVPSTPPTPSPSTPPT
PSPSCAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDG
VEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTI
SKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNY

 ${\tt KTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPG} \\ {\tt K}$

51. G28-1 scFv VHL11S (SSS-S)H WCH2 WCH3

5 Nucleotide sequence:

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a agett g ccgccat g g tatcca caget cagtt cett g g g tt g ctg ctg t g g ctg ag g t g g cag at g t g acat ccag at g act caget g g ctg acat ccag at g act caget g ctg act g ctg aat cag cagaa a cag ggaa a a at ct cet cag et cet gg tet et tt tt geaa a a a acct tag cagaa gg t g t g ceat ca a g gt te a g te a ga a comment of the stage of tgtggatcaggcacacagttttctctgaagatcagcagcctgaagattctggaagttatttctgtcaacatcattccgataat10 cattcactggctacaatatgaactgggtgaagcagaataatggaaagagccttgagtggattggaaatattgatccttattatggtggt actacetacaaceggaagttcaagggcaaggccacattgactgtagacaaatcctccagcacagcctacatgcagctcaagagtct gacatet gaggactet geag tetatta et gt geaa gateg gecetat ggacta et ggggte aa ggaacete ag te accept et en de state gaggactet geag te accept et en de state gaggactet gegen gacatet gaggactet gegen gacatet gaggactet gag15 ttet gate aggage ee aaatet tet gacaaaa act caca cate cocace gteet eage acet gaacteet ggggggace gte agtet the state of thgaccet gagg tea agt tea act gg tacgt gg ac gg tg gagg tg cata at gc caa gacaa ag ce ge gg gagg ag cagt acaa gacaa ag ce gg gagg ag cagt acaa gacaa ag ce ge gg gagg ag cagt acaa gacaa ag ce ge gg gagg ag cagt acaa gacaa ag ce gg gagg ag cagt acaa gacaa gacaa ag ce gg gagg ag cagt acaa gacaa gacaa ag ce gg gagg ag cagt acaa gacaa gacacag cac g tac c g t g t cag c g t c c t cac c g t c c t g cac c a g g a c t g c a a g g a c t g c a a g g a c t g c a a g g a c t g c a a g g a c t g c a a g g a c t g c a a g g a c t g c a a g g a c t g c a a g g a c t g c a a g g a c t g c a a g g a c a g g a c t g c a a g g a c t g c a a g g a c t g c a a g g a c a g g a c t g c a a g g a c a g g aan agccctcccagcccccatcg agaaaacaatctccaa agccaa agggcagccccg agaaccacaggtg tacaccctgccccc20 $atcccggg at gagctgaccaagaaccaggt \^{c} agcctgacctgcctggtcaaaggcttctatcccagcgacatcgccgtggagtgg$ gagag caatggg cag cag gagaac aacta caa gac cac g cct ccc gt get ggac tee gac g get cct t ct t cac ag caa gagaa gagaa caa gac cac g cct ccc gt get ggac tee gac g gagaa caa caa gac cac g cct ccc gt get ggac tee gac g gac gagaa caa caa gac cac g cct ccc gt g ct g gac tee g gac g cac g cacctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgc agaagagcctctccctgtctccgggtaaatgatctaga

25 Amino acid sequence:

MVSTAQFLGLLLWLTGGRCDIQMTQSPASLSASVGETVTITCRTSENVYSYLAW YQQKQGKSPQLLVSFAKTLAEGVPSRFSGSGSGTQFSLKISSLQPEDSGSYFCQHHS DNPWTFGGGTELEIKGGGGSGGGGSGGGGSSAVQLQQSGPESEKPGASVKISCKA SGYSFTGYNMNWVKQNNGKSLEWIGNIDPYYGGTTYNRKFKGKATLTVDKSSST

30 AYMQLKSLTSEDSAVYYCARSVGPMDYWGQGTSVTVSSDHDQEPKSSDKTHTSP PSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVE VHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISK AKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKT TPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

52. G28-1 scFv VHL11S (CSS-S)H WCH2 WCH3

Nucleotide sequence:

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Amino acid sequence:

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MVSTAQFLGLLLWLTGGRCDIQMTQSPASLSASVGETVTITCRTSENVYSYLAW YQQKQGKSPQLLVSFAKTLAEGVPSRFSGSGSGTQFSLKISSLQPEDSGSYFCQHHS DNPWTFGGGTELEIKGGGGSGGGGSGGGGSSAVQLQQSGPESEKPGASVKISCKA SGYSFTGYNMNWVKQNNGKSLEWIGNIDPYYGGTTYNRKFKGKATLTVDKSSST AYMQLKSLTSEDSAVYYCARSVGPMDYWGQGTSVTVSSDQEPKSCDKTHTSPPSS APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

53. G28-1 scFv VH L11S (CSC-S)H WCH2 WCH3

Nucleotide sequence:

20 agteteeageeteeetatetgeatetgtgggagagactgteaceateaeatgtegaaeaagtgaaaatgtttaeagttatttggettggt atcagcagaaacagggaaaatctcctcagctcctggtctcttttgcaaaaaccttagcagaaggtgtgccatcaaggttcagtggca gtggateaggeacacagttttetetgaagateageageetgeageetgaagattetggaagttatttetgteaacateatteegataat egt cag c g st cag c t g cag cag t c t g a c t g a c t g a c t g cag c t t cag t g a a g a t t c t g c a a g c t t c t g t a c t c a c t c a c t c a c t c a c t c a c t c a c t c a c t c a c c a c c a c c a c c a c c a c c a c c a c c a c c a c c a c c c a c a c c a c a c c a c a c c a c25 cattcactggctacaatatgaactgggtgaagcagaataatggaaagagcettgagtggattggaaatattgatcettattatggtggt actacctaca accgga agtica agg cca caft gact gtaga can at cct ccag cacag cct a cat gcag ct caa gag tct act gcag cacag cct acat gcag ctca agg ctca agg cct acat gcag ctca acat gcag ctca agg cct acat gcag ctca acagacatetgaggactetgeagtetattaetgtgeaagateggteggeeetatggactaetgggteaaggaaceteagteaeegtete ttotgat cag gag ceca a a tett g t gaca a a a ctea caca cate t cac e g t get cag cac e t ga a cte t g g t g a ce t t cac e g t g t cag cac e t g a a ctea g g t g a ce t t cac e g t g t ca g cac e t g a c caca e t caca e t caca e g t caca e t cacctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtggtggtggtggacgtgagccacgaag 30 accet gagg tea agt tea act gg ta eg t gg ac gg t gg ag gg t ge at a at gc ea ag ac a ag ac ag ag ag ag ag ag ta ea ac act gg ta eg ta ea act gg ta eg ta ea act gg ta eg ta ea act gg ta eg taagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaaca aagccctcccagccccatcgagaaaacaatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccca tcccggatgagctgaccaagaaccaggtcagcctgacctgctggtcaaaggcttctatccaagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcetcccgtgctggactccgacggctccttcttcctctacagcaag 35 ctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga

Amino acid sequence:

- MVSTAQFLGLLLLWLTGGRCDIQMTQSPASLSASVGETVTITCRTSENVYSYLAW

 40 YQQKQGKSPQLLVSFAKTLAEGVPSRFSGSGSGTQFSLKISSLQPEDSGSYFCQHHS
 DNPWTFGGGTELEIKGGGGSGGGGSGGGGSSAVQLQQSGPESEKPGASVKISCKA
 SGYSFTGYNMNWVKQNNGKSLEWIGNIDPYYGGTTYNRKFKGKATLTVDKSSST
 AYMQLKSLTSEDSAVYYCARSVGPMDYWGQGTSVTVSSDQEPKSCDKTHTSPPC
 SAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEV
- 45 HNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKA KGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP PVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

50 54. G28-1 scFv VH L11S (SSC-P)H WCH2 WCH3

Nucleotide sequence:

angett g ceg ceat g g t at ceacage te a gette ett g g g t t g ceg cet g t g g ceat g t g g ceat g t g ceacage t g g ceat g t g ceacage t g g ceat g t g ceacage t g ceacageagtete cage ctcce fatet geatet g t g g agaga ct g teace at eac at g tegaa caa g t g aa aa t g t t t ac g t t at t t g g t t g t ac a t g t cac at g t cac at g t g aa caa g t g aa aa t g t t t ac g t t at t t g g t t g t cac at g t cac at g t g aa caa g t g aa aa t g t t t ac g t t at t t g g t t g t ac a t g t g ac a ca g t g aa aa t g t t t ac g t t ac g t cac at g t g aa caa g t g aa aa t g t t t ac g t t ac g t cac at g t g aa caa g t g aa aa t g t t t ac g t t ac g t cac ac a t g t cac ac a g t g aa aa a t g t t t ac g t t ac g t cac ac a g t g aa aa a t g t t ac g t t ac g t cac ac a g t g aa aa a t g t t ac g t ac a cac a g t g aa aa a t g t t ac g t ac a cac a g t g aa aa a t g t t ac g t ac a cac a g t g aa aa a t g t t ac a cac a g t g aa aa a t g t t ac a cac a g t g aa aa a t g t t ac a cac a g t g aa aa a t g t t ac a cac a g t g aa aa a t g t t ac a cac a g t g aa aa a t g t t ac a cac a g t g aa aa a t g t t ac a cac a g t g aa aa a t g t t ac a cac a g t g aa a cac a g t g ac a cac a cac a cac a g ac a cac a cacgtggatcaggcacacagttttctctgaagatcagcagcctgcagcctgaagattctggaagttatttctgtcaacatcattccgataat cattcactggctacaatatgaactgggtgaagcagaataatggaaagagccttgagtggattggaaatattgatccttattatggtggt actace ta caacegga agtte a aggee a aggee acattga et ga caa a teet ceage acage et a catge agget caa gag te ta catge aggee aggee acat gag aggee aggee acat gag aggee agggacatet gaggactet gcagtet attact gt geaagateggt eggee ctat ggatet act ggggt ea ggaacet cagte accept et each gaggactet gaggac10 ttetgateaggageeeaaatettetgacaaaacteacacateceeacegtgeeeageacetgaacteetggggggacegteagtett cetettececeaaaacccaaggacacceteatgateteceggacccetgaggteacatgegtggtggtggacgtgagccacgaa cagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtctccaac aaagccctcccagccccatcgagaaaacaatctccaaagccaaagggcagccccgagaaccacaggtgtacaccctgcccc 15 gagag caat ggg cag ccg gagaac aactac aagac cac gcct cccg t gct ggac tcc gac ggct cct tct tcct ctac ag caagagaagagcctctccctgtctccgggtaaatgatctaga

20 Amino acid sequence:

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MVSTAQFLGLLLWLTGGRCDIQMTQSPASLSASVGETVTITCRTSENVYSYLAW YQQKQGKSPQLLVSFAKTLAEGVPSRFSGSGSGTQFSLKISSLQPEDSGSYFCQHHS DNPWTFGGGTELEIKGGGGSGGGGSGGGGSSAVQLQQSGPESEKPGASVKISCKA SGYSFTGYNMNWVKQNNGKSLEWIGNIDPYYGGTTYNRKFKGKATLTVDKSSST AYMQLKSLTSEDSAVYYCARSVGPMDYWGQGTSVTVSSDQEPKSSDKTHTSPPCP APELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH NAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTIPP VLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

II. 54. HCTLA4 HIGG1 (SSS-S)H P238SCH2 WCH3

Nucleotide sequence:

Amino acid sequence:

MACLGFQRHKAQLNLAARTWPCTLLFFLLFIPVFCKAMHVAQPAVVLASSRGIAS 50 FVCEYASPGKATEVRVTVLRQADSQVTEVCAATYMTGNELTFLDDSICTGTSSGN

QVNLTIQGLRAMDTGLYICKVELMYPPPYYLGIGNGTQIYVIDPEPCPDSDQPKSSD KTHTSPPSSAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWY VDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPI EKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPE

5 NNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSL SPGK

55. Fe2-2 VL

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Nucleotide sequence:

10 gttgttaagettgeegecatggatteacaggeecaggttettatgttaetgetgetatgggtatetggtaectgtggggaeattgtgatg
teacagtetecatecteectagetgtgteagttggagagaggttetatgagetgeaagteeagteaggeettttatataateacaat
caaaagaactaettggeetggtaecageagataecagggeagteteetaaaetgetgatttaetgggeateeactagggaatetgg
ggteectgategetteacaggeagtggatetgggaeagattteaeteteaceateageagatgaaggetgaagaeetggeagttta
ttaetgteageaatattataeetateeteecaegtteggaggtggeaecaagetggaaataaaaggtggeggtggetegggggg
15 gtgggtegggtggegggggageteg

Amino acid sequence:

MDSQAQVLMLLLLWVSGTCGDIVMSQSPSSLAVSVGEKVSMSCKSSQSLLYNHN QKNYLAWYQQIPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISRVKAEDLA VYYCQQYYTYPPTFGGGTKLEIKGGGGSGGGGSGGGSS

56. FC2-2VH

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Nucleotide sequence:

Gggagetegeagttgaagtgaagteaggacetggeetggtiggegeeeteacagageetgtecateacatgeacegtetea gggtteteattaacegtetatggtgttaactgggttegeeagcetecaggaaagggtetggaetgggaatgatatggggtgat ggaagcacagactataatteageteteaaateeagaetgageateagtaaggacaacteeaagageeaagtttettaaaaatggae agtetacaaactgatgacacageeaggtactaetgtgeeagagateactatggtacccactatgetatggactactggggleaagga aceteagteacegteteetetgateag

30 Amino acid sequence:

 $\label{thm:condition} GSSQVQLKESGPGLVAPSQSLSITCTVSGFSLTVYGVNWVRQPPGKGLDWLGMIW\\ GDGSTDYNSALKSRLSISKDNSKSQVFLKMDSLQTDDTARYYCARDHYGTHYAM\\ DYWGQGTSVTVSSDQ$

35 **57. FC2-2scFv**

Nucleotide sequence:

Amino acid sequence:

MDSQAQVLMLLLLWVSGTCGDIVMSQSPSSLAVSVGEKVSMSCKSSQSLLYNHN 50 QKNYLAWYQQIPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISRVKAEDLA VYYCQQYYTYPPTFGGGTKLEIKGGGGSGGGSGGGGSSQVQLKESGPGLVAPSQ 10

15

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SLSITCTVSGFSLTVYGVNWVRQPPGKGLDWLGMIWGDGSTDYNSALKSRLSISK DNSKSQVFLKMDSLQTDDTARYYCARDHYGTHYAMDYWGQGTSVTVSSDQ

58. FC2-2 VHL11S

5 Nucleotide sequence:

gggageteteaggtgeagttgaaggagteaggacetggeteggtggegeeeteacagageetgtecateacatgeacegteteag ggtteteattaacegtetatggtgttaactgggttegecageeteeaggaaagggtetggactggetgggaatgatatggggtgatg gaageacagactataatteageteteaaateeagaetgageateagtaaggacaacteeaagageeaagttttettaaaaatggaca gtetacaaactgatgacaaggacaagtactactgtgeeagagateactatggtaeccactatgetatggactactggggteaaggaa ceteagteacegteteetetgateag

Amino acid sequence:

(GSS)QVQLKESGPGSVAPSQSLSITCTVSGFSLTVYGVNWVRQPPGKGLDWLGMI WGDGSTDYNSALKSRLSISKDNSKSQVFLKMDSLQTDDTARYYCARDHYGTHYA MDYWGQGTSVTVSSDQ

59. FC2-2 VH L11S scFv

Nucleotide sequence:

- 30 Amino acid sequence:

MDSQAQVLMLLLLWVSGTCGDIVMSQSPSSLAVSVGEKVSMSCKSSQSLLYNHN QKNYLAWYQQIPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISRVKAEDLA VYYCQQYYTYPPTFGGGTKLEIKGGGGSGGGGSGGGGSSQVQLKESGPGSVAPSQ SLSITCTVSGFSLTVYGVNWVRQPPGKGLDWLGMIWGDGSTDYNSALKSRLSISK

35 DNSKSQVFLKMDSLQTDDTARYYCARDHYGTHYAMDYWGQGTSVTVSSDQ

60. FC2-2 (SSS-S)H WCH2 WCH3

Nucleotide sequence:

- 50 gtcacatgcgtggtggtggacgtgagccacgaagaccetgaggtcaagttcaactggtacgtggacggcgtggaggtgcataat gccaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggct

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Amino acid sequence:

 $\label{eq:mdsqaqvlmlllwvsgtcgdivmsqspsslavsvgekvsmsckssqsllynhn Qknylawyqqipqqspklliywastresgvpdrftgsgsgtdftltisrvkaedla$

- 10 VYYCQQYYTYPPTFGGGTKLEIKGGGGSGGGSGGGGSGGGSSQVQLKESGPGLVAPSQ SLSITCTVSGFSLTVYGVNWVRQPPGKGLDWLGMIWGDGSTDYNSALKSRLSISK DNSKSQVFLKMDSLQTDDTARYYCARDHYGTHYAMDYWGQGTSVTVSSDQEPK SSDKTHTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA
- 15 LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ KSLSLSPGK

61. FC2-2 VHL11S (SSS-S)H WCH2 WCH3

- 20 Nucleotide sequence:

- agccccgagaaccacaggtgtacaccctgccccatcccgggatgagctgaccaagaaccaggtcagcctgacctgctggtca aaggcttctatccaagcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctccgtg ctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctc cgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctaga
- 40 Amino acid sequence:
 - MDSQAQVLMLLLLWVSGTCGDIVMSQSPSSLAVSVGEKVSMSCKSSQSLLYNHN QKNYLAWYQQIPGQSPKLLIYWASTRESGVPDRFTGSGSGTDFTLTISRVKAEDLA VYYCQQYYTYPPTFGGGTKLEIKGGGGSGGGSGGGGSSQVQLKESGPGSVAPSQ SLSITCTVSGFSLTVYGVNWVRQPPGKGLDWLGMIWGDGSTDYNSALKSRLSISK
- DNSKSQVFLKMDSLQTDDTARYYCARDHYGTHYAMDYWGQGTSVTVSSDQEPK SSDKTHTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF NWYVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKA LPAPIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESN GQPENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQ
- 50 KSLSLSPGK

62. UCHL-1 VH

Nucleotide sequence:

atgggcaggcttacttcttcattcctgctactgattgttcctgcatatgtcctctcccagattactctgaaagagtctggccctgggatctt gcagccctcccagaccctcagtctgacttgttcttctctgggttttcactgaccacttatggtataggagtaggttggattcgtcagcct ccagggaagggtctggagtggctgacacacatttggtggaatgataataagtactataacacagccctgaggagccggctcacaa tctccaaggattcctccaacaaccaagtactctcaagatcgccaatgtggacactgcagataccgccacatactactgtctctacg gctacacttactggggccaagggactctggtcactgtctctgca

Amino acid sequence:

10 MGRLTSSFLLLIVPAYVLSQITLKESGPGILQPSQTLSLTCSFSGFSLTTYGIGVGWIR QPPGKGLEWLTHIWWNDNKYYNTALRSRLTISKDSSNNQVLLKIANVDTADTAT YYCLYGYTYWGQGTLVTVSA

63. UCHL-1 VL

15 Nucleotide sequence:

20 tggacgttcggtggaggcaccaagctggaaatcaaa

Amino acid sequence:

MKLPVRLLVLMFWIPASISDVVMTQTPLSLPVSLGDQASISCRSSQSLLYSNGNTYL HWYLQKPGQSPKLLIYKLSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCS QSTHVPWTFGGGTKLEIK

64. UCHL-1 scFv

25

Nucleotide sequence:

- ttggtggaatgataataagtactataacacagccetgaggagccggctcacaatctccaaggattcctccaacaaccaagtactcct
 caagatcgccaatgtggacactgcagataccgccacatactactgtctctacggctacacttactggggccaagggactctggtca
 ctgtctctgctgatca
- 40 Amino acid sequence:

MKLPVRLLVLMFWIPASISDVVMTQTPLSLPVSLGDQASISCRSSQSLLYSNGNTYL HWYLQKPGQSPKLLIYKLSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCS QSTHVPWTFGGGTKLEIKDGGGSGGGGGGGGGGSSQITLKESGPGILQPSQTLSLTCS FSGFSLTTYGIGVGWIRQPPGKGLEWLTHIWWNDNKYYNTALRSRLTISKDSSNN

45 QVLLKIANVDTADTATYYCLYGYTYWGQGTLVTVSAD

65. UCHL-1 VH I11SL12S

Nucleotide sequence:

50 gggageteteagattaetetgaaagagtetggeeetgggatettgeageeeteeagaceeteagtetgaettgttetttetetgggttt teaetgaeeacttatggtataggatggattggattegteageeteeagggaagggtetggagtggetgaeacacatttggtggaat

5 Amino acid sequence:

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(GSS)QITLKESGPGSSQPSQTLSLTCSFSGFSLTTYGIGVGWIRQPPGKGLEWLTHIW WNDNKYYNTALRSRLTISKDSSNNQVLLKIANVDTADTATYYCLYGYTYWGQGT LVTVSAD

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66. UCHL-1 scFv VH L11S

Nucleotide sequence:

Amino acid sequence:

25 MKLPVRLLVLMFWIPASISDVVMTQTPLSLPVSLGDQASISCRSSQSLLYSNGNTYL HWYLQKPGQSPKLLIYKLSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCS QSTHVPWTFGGGTKLEIKDGGGSGGGGGGGGGGSGQITLKESGPGSSQPSQTLSLTC SFSGFSLTTYGIGVGWIRQPPGKGLEWLTHIWWNDNKYYNTALRSRLTISKDSSNN QVLLKIANVDTADTATYYCLYGYTYWGQGTLVTVSAD

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67. UCHL-1 scFv (SSS-S)H WCH2 WCH3

Nucleotide sequence:

gttgttaagettgeegeeatgaagttgeetgttaggetgttggtgetgatgttetggatteetgetteeateagtgatgttgtgatgaeeea a act ccaet ctee ctg cctg teag tett gg agate aggeet ceatet ctt ge agate tagte agae cette tta eagta at gg aa actee actee to the contract of the contract ofacct attta cattggta acctg cag aag c cag ge cag tete caa aact cet gate ta caa acttte caa ceg atttte t g g g te cea g a constitution of the consticaggt t cag t g g a t cag g g a cag a t t t cacac t caa g a t cag cag a g t g a g g a t c t g g g a g t t t a t t t c t g c t cag g t g a g g a t c t g g g a g t t t a t t t c t g c t cag g t g a g g a t c t g g g a g t t t a t t t c t g c t cag g t g a g g a t c t g g g a g t t t a t t t c t g c t cag g a g t g a g g a t c t g g g a g t t t a t t t c t g c t cag g a g t g a g g a t c t g g g a g t t a t t t c t g c t cag g a g t g a g g a t c t g g g a g t t t a t t t c t g c t cag g a g t g a g g a t c t g g g a g t t t a t t t c t g c t cag g a g t g a g g a t c t g g g a g t t t a t t t c t g c t cag g a g t g a g g a t c t g g g a g t t t a t t t c t g c t cag g a g t c t g g g a g t t t a t t t c t g c t cag g a g t t t a t t t c t g c t cag g a g c t g a g g a t c t g g g a g t t t a t t t c t g c t cag g a g c t g a g g a t c t g g g a g t t t a t t t c t g c t cag g a g c t g a g g a t c t g g g a g c t g a g g a t c t g g g a g c t g a g g a t c t g g g a g c t g a g g a t c t g g g a g c t g a g g a t c t g g g a g c t g a g g a t c t g g g a g c t g a g g a t c t g g g a g c t g a g g a t c t g g g a g c t g a g g a t c t g g g a g c t g a g g a t c t g g g a g c t g a g g a t c t g g a g c t g a g g a c t g a g a g c t g a g g a c t g a g a g c t g a g g a c t g a g a g c t g a g at caa agta cacat gtt cegt gga eg t teggt gga gg cacca ag c t gga aat caa ag at gge gg t gg c tegg gg t gg t teg ga tetter to a significant of the contract oggaggaggtgggagctctcagattactctgaaagagtctggccctgggatcttgcagccctccagaccctcagtctgacttgttctt tetetgggttttcactgaccacttatggtataggagtaggttggattcgtcagcctccagggaagggtctggagtggctgacacacatttggtggaatgataataagtactataacaagccctgaggagccggctcacaatctccaaggattcctccaacaaccaagtactcctcaagategccaatgtggacactgcagatacegccacatactactgtetetaeggetacacttaetggggccaagggactetggtca ctg tctctg at caggage ceaa at cttctg acaa aact cacacacaccac cg tcctcag cacctg gactcctg gg tgg accgtgtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggtc tecaacaaageeteccageeccategagaaaaccatetecaaageeaaagggaageecegagaaceacaggtgtacaccet geocecate ceggg at gaget gacea agaac cagg teage et gacet get gatea a agget teatacca age gacate geographic gateau agget ggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctccgtgctggactccgacggctccttcttcctctac agca agct caceg tgga caagag cag gtgg cag cag gggaacgt ctt ctc at get ceg tgat ge at gag get ctg caca accaetacacgcagaagagcctctccctgtctccgggtaaatgatctaga

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Amino acid sequence:

MKLPVRLLVLMFWIPASISDVVMTQTPLSLPVSLGDQASISCRSSQSLLYSNGNTYL
HWYLQKPGQSPKLLIYKLSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCS
QSTHVPWTFGGGTKLEIKDGGGSGGGGSGGGGSSQITLKESGPGILQPSQTLSLTCS
FSGFSLTTYGIGVGWIRQPPGKGLEWLTHIWWNDNKYYNTALRSRLTISKDSSNN
QVLLKIANVDTADTATYYCLYGYTYWGQGTLVTVSADQEPKSSDKTHTSPPSSAP
ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA
KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ
PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL
DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

68. UCHL-1 scFv VHL11S (SSS-S)H WCH2 WCH3

15 Nucleotide sequence:

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gttgttaagcttgccgccatgaagttgcctgttaggctgttggtgctgatgttctggattcctgcttccatcagtgatgttgtgatgacccaa act ccact ctcct geet gt cag tett gg agat cag geet ccat ctct t ge agat ctag te agat cag age ctt ctt t acag ta at gg aa act ccact ctc tett ge agat ctag tett ge agat ctag te agat cag agat ctag tett ge agat ctacct attta cattggt acctg cag aag c cag g c cag tete caa aa act cet g at et a caa actt te caa ceg at ttte t g g g g te cea g a constant to the constant to tht caa ag taca cat gtt ccg tgg acgtt cgg tgg ag gcacca ag ctgg aa at caa ag at gg cgg tgg tcg gg tgg tgg tgg at ctgg according to the contract of the contracggaggaggtggaggctctcagattactctgaaagagtctggccctgggagctcccagaccctcagacctcagtctgacttgttctttctctgggttttcactgaccacttatggtataggagtaggttggattcgtcagcctccagggaagggtctggagtggctgacacacttatggtataggagtaggttggattcgtcagcctccagggaagggtctggagtggctgacacacttatggtataggagtaggttggattcgtcagcctccagggaagggtctggagtggctgacacacttatggtataggagtaggttggattcgtcagcctccagggaagggtctggagtggctgacacacttatggtataggagtaggttggattcgtcagcctccagggaagggtctggagtggctgacacacttatggtataggagtaggattggattcgtcagcctccagggaagggtctggagtaggattggattcgtcagcctccagggaagggtctggagtaggattggattaggattggattcgtcagcacacacttatggattaggatttggtggaatgataataagtactataacaagccctgaggagccggctcacaatctccaaggattcctccaacaaccaagtactcact g to tot g cigate a ga a goe caa a a tot coe a cate coe a coefficient a grant coefficient and a constraint of the coefficient and the coeffit cag tette ctette cece caa aa acce caa ag acce cte at gate te ceg gae cect gag g te acat geg t g g te gag te central constraints and the constraints and the constraints are constraints are constraints and the constraints are constraints and the constraints are constraints are constraints and the constraints are constraints are constraints are constraints and the constraints are constraints are constraints are constraints are constraints and the constraints are constraints are constraints are constraints are constraints and constraints are constraints are constraints are constraints are constraintagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagtacaagtgcaaggt $\tt ctccaacaaagccctcccagcccccatcgagaaaaccatctccaaagccaaagggcagccccgagaaccacaggtgtacaccc$ ggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtettetcatgctccgtgatgcatgaggctetgcacaacca ctacacgcagaagagcctctccctgtctccgggtaaatgatctagaa

35 Amino acid sequence:

MKLPVRLLVLMFWIPASISDVVMTQTPLSLPVSLGDQASISCRSSQSLLYSNGNTYL HWYLQKPGQSPKLLIYKLSNRFSGVPDRFSGSGSGTDFTLKISRVEAEDLGVYFCS QSTHVPWTFGGGTKLEIKDGGGSGGGGGGGGGGGSSQITLKESGPGSSQPSQTLSLTC SFSGFSLTTYGIGVGWIRQPPGKGLEWLTHIWWNDNKYYNTALRSRLTISKDSSNN QVLLKIANVDTADTATYYCLYGYTYWGQGTLVTVSADQEPKSSDKTHTSPPSSAP ELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNA KTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQ PREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVL DSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLSPGK

69. 5B9 VH L11S

Nucleotide sequence:

gggagctctcaggtgcagctgaagcagtcaggacctggctcagtgcagtcctcacagagcctgtccatcacctgcacagtctctg gtttctcattaactacctatgctgtacactgggttcgccagtctccaggaaagggtctggagtggctggagtgatatggagtggtgg aatcacagactataatgcagctttcatatccagactgagcatcaccaaggacgattccaagagccaagttttctttaaaatgaacagtc

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WO 2005/017148 PCT/US2003/041600

tg caaccta at gacacag ccatttat tactg tg ccagaa at gg gg gt gataactac cct tattactat gctat gg actact gg gg tcaa gg aacct cag tcac gct ccct cag

Amino acid sequence:

5 (GSS)QVQLKQSGPGSVQSSQSLSITCTVSGFSLTTYAVHWVRQSPGKGLEWLGVI WSGGITDYNAAFISRLSITKDDSKSQVFFKMNSLQPNDTAIYYCARNGGDNYPYY YAMDYWGQGTSVTVSS

10 73. 5B9 VH L11S scFv

Nucleotide sequence:

Amino acid sequence:

MRFSAQLLGLLVLWIPGSTADIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITY
LYWYLQKPGQSPQLLIYQMSNLASGVPDRFSSSGSGTDFTLRISRVEAEDVGVYYC
AQNLELPLTFGAGTKLELKRGGGGSGGGGGGGGGSSQVQLKQSGPGSVQSSQSLSI
TCTVSGFSLTTYAVHWVRQSPGKGLEWLGVIWSGGITDYNAAFISRLSITKDDSKS
QVFFKMNSLQPNDTAIYYCARNGGDNYPYYYAMDYWGQGTSVTVSS

50 500 E TOTAL

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70. 5B9 scFv VHL11S (SSS-S)H WCH2 WCH3

Nucleotide sequence:

a agett g ceg ceat g aggtt ctet g ctet g g g ct g ctt g t g at ceet g g at ceat g cag at at t g t g at g ac g can a get t g c g at ceat g cag at at t g t g at g ac g can a g c t g cag at at t g t g at g ac g can a g c t g cag at at t g t g at g ac g can a g c t g cag at at t g t g at g ac g can a g c t g cag at at t g t g at g ac g can a g can aggctgcattctccaatccagtcactcttggaacatcagcttccatctcctgcaggtctagtaagagtctcctacatagtaatggcatcacgggtggcggcgggagctctcaggtgcagctgaagcagtcaggacctggctcagtgcagtcctcacagagcctgtccatcacctgcacagtctctggtttctcattaactacctatgctgtacactgggttcgccagtctccaggaaagggtctggagtggctgggagtgatatggagtggtggaatcacagactataatgcagctttcatatccagactgagcatcaccaaggacgattccaagagccaagttttctttaaaatgaacagtctgcaacctaatgacacagccatttattactgtgccagaaatgggggtgataactacccttattactatgctatgga ctactggggtcaaggaacctcagtcaccgtctcctctgatcaggagcccaaatcttctgacaaaactcacacatccccaccgtcctc agcacctgaactcctgggtggaccgtcagtcttcctcttccccccaaaacccaaggacaccctcatgatctcccggacccctgagg tcacatgcgtggtggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgcacgtggacgtggacgtggaggtgcataatgcacgtggacgtggacgtggaggtgcataatgcacgtggacgtggacgtggaggtgcataatgcacgtgaggtggacgtggacgtgaggtgcataatgcacgtgaggtgaaggaaggtgaagaaggaagaaggaacaagacaaagccgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaalggcaaggagtacaagtgcaaggtetecaacaaageceteecageececategagaaaaceatetecaaaggcaaagggcag ccccg agaac cacaggt g tacaccctg cccccatcccgg g at gagctg accaagaac caggt cagcctg acctg acctg acctg acctg acctaggt can also be a considered according to the considered aggactccgacggctccttcttcctctacagcaagctcaccgtggacaagagcaggtggcagcaggggaacgtcttctcatgctccgtgatgcatgaggctctgcacaaccactacacgcagaagagcctctccctgtctccgggtaaatgatctagag

Amino acid sequence:

MRFSAQLLGLLVLWIPGSTADIVMTQAAFSNPVTLGTSASISCRSSKSLLHSNGITY
LYWYLQKPGQSPQLLIYQMSNLASGVPDRFSSSGSGTDFTLRISRVEAEDVGVYYC
AQNLELPLTFGAGTKLELKRGGGGSGGGGSGGGGSSQVQLKQSGPGSVQSSQSLSI
TCTVSGFSLTTYAVHWVRQSPGKGLEWLGVIWSGGITDYNAAFISRLSITKDDSKS
QVFFKMNSLQPNDTAIYYCARNGGDNYPYYYAMDYWGQGTSVTVSSDQEPKSS
DKTHTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW
YVDGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPA
PIEKTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQP

10 ENNYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLS LSPGK

15 76. 2H7 scFv VH L11S (SSS-S)H P238SCH2 WCH3

Nucleotide sequence:

a agett g ceg ceat g g att tt caa g t g cag att tt cagett cet g ctaat cag t g ct t cag t cat a att g ceag ag g a caa att g t t ct ctag t cat a description of the companion ofcccag tete cag caate ct geate te cag gg gag aa gg teacaat gaet t geag ge cag et caa gt gt aa gt ta cat geact te cag gg gag aa gg teacaat gaet t geag geag et caa gt geact ge20 ta acceace acg t cgg tgctgggace aage tggage tgaa agatggcgg tggctcgggcggtggtctggage tggage tggageteteaggettatetacageagtetggggetgagteggtgaggeetgggggeeteagtgaagatgteetgcaaggettetgge tacacatttaccagttacaatatgcactgggtaaagcagacacctagacagggcctggaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagctatttatccaggaaatggattggagcaggacaggaatggattggagcaggaatggattggagcaggaatggattggagcaggaatggattggagcaggaatggaatggattggagcaggaatggattggagcaggaatggaatggattggagcaggaatggacage etga catetga agae to tgegg to tatt to tgtg can gag tg tg tactat ag taac to tta etg gag act to tgt gag to tatt to tgt gag agae to tgt gag to tatt gag to tatt25 agggaccacggtcaccgtctcttctgatcaggagcccaaatcttctgacaaaactcacacatccccaccgtcctcagcacctgaact $\verb|cotggggggategtcagtettcctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtgg$ cgcggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggagta ca agtg ca aggtc tecca aca aag ecc tecca ge cecca tegagaa aa ca at et cea aag ecca aag ge ca ge cecegagaa cecca agge ca agge ca agge ca aag ecca aag ec30 a caggitg tacaccct g cocccate ccgg g at gagetg accaa gaaccag g teagect g acct g cct g g teaa ag get tetate cccarried accept g aagegacategeegtggagtgggagageaatgggeageeggagaacaactacaagaccaegceteeegtgetggacteegaeg getetgeacaaccactacacgcagaagagceteteeetgteteegggtaaatgatetaga

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PGK

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Amino acid sequence:
MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGSSQAYLQQSGAESVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
THTSPPSSAPELLGGSSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS

78. 2H7 scFv VH L11S (SSS-S)H WCH2 WCH3

Nucleotide sequence:

aagettgeegecatggatttteaagtgeagatttteagetteetgetaateagtgetteagteataattgeeagaggaeaaattgttetet eccagteteeageaateetgtetgeateteeaggggagaaggteacaatgaettgeagggeeageteaagtgaagttaeatgeaet

ggtaccagcagaagccaggatcctcccccaaaccctggatttatgccccatccaacctggcttctggagtccctgctcgcttcagtg g cagtgggtctgggacctcttactctctcacaatcagcagagtggaggctgaagatgctgccacttattactgccagcagtggagttttaacccaccacgtteggtgctgggaccaagctggagctgaaagatggcggtggctegggcggtggtggatctggaggaggtg ggagcteteaggettatetaeageagtetggggetgagteggtgaggeetggggeeteagtgaagatgteetgeaaggettetgge ggtgataetteetaeaateagaagtteaagggeaaggeeacaetgaetgtagaeaaateeteeageaeageetaeatgeageteag cctggggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtgg 10 tggtggacgtgagccacgaagaccctgaggtcaagttcaactggtacgtggacggcgtggaggtgcataatgccaagacaaagc egegggaggagcagtacaacagcacgtaccgtgtggtcagcgtcetcaccgtcctgcaccaggactggctgaatggcaaggag tacaagtgcaaggtetecaacaaagcceteccagececcategagaaaacaatetecaaagccaaagggcagececgagaace a caggtg tacaccet g ccccatcceg g at gagetg accaa g accagg te agect g acct g cet g g te a a agget te tate cet g accept g acceptagcgacatcgccgtggagtgggaggaacaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacg 15 get cet tet te cet caage aa get ea cegt grac aa gag ea geg gaa e get et te te cat get ee geg gat geat gag gag ea geg gaa e get et te te cat get ee geg gat geat gag gag ea geg gag ea geggetet geaca accae cae acae geaga agag cetet ceet gtet ceggg ta a at gate taga

Amino acid sequence:

WO 2005/017148

MDFQVQIFSFLLISASVIIARGQIVLSQSPAILSASPGEKVTMTCRASSSVSYMHWY
QQKPGSSPKPWIYAPSNLASGVPARFSGSGSGTSYSLTISRVEAEDAATYYCQQWS
FNPPTFGAGTKLELKDGGGSGGGGSGGGGSSQAYLQQSGAESVRPGASVKMSCK
ASGYTFTSYNMHWVKQTPRQGLEWIGAIYPGNGDTSYNQKFKGKATLTVDKSSS
TAYMQLSSLTSEDSAVYFCARVVYYSNSYWYFDVWGTGTTVTVSSDQEPKSSDK
THTSPPSSAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYV
DGVEVHNAKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIE
KTISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPEN
NYKTTPPVLDSDGSFFLYSKLTVDKSRWQQGNVFSCSVMHEALHNHYTQKSLSLS
PGK

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79. 2H7 scFv VH L11S (CSS-S)H WCH2 WCH3

Nucleotide sequence:

ccag to tccag caatcet g to tgcatctccag g g aga agg tcaca at gact tgcag g g ccag ctcaa g t g tacat g cact g cacat g cggtaccagcagaagccaggatcctcccccaaaccctggatttatgccccatccaacctggcttctggagtccctgctcgcttcagtg tacacatttaccagttacaatatgcactgggtaaagcagacacctagacagggcctggaatggattggagctatttatccaggaaat agggaccacggtcaccgtctcttctgatcaggagcccaaatcttgtgacaaaactcacacactccccaccgtcctcagcacctgaact cctggggggaccgtcagtcttcctcttcccccaaaacccaaggacaccctcatgatctcccggacccctgaggtcacatgcgtgg cgcgggaggagcagtacaacagcacgtaccgtgtggtcagcgtcctcaccgtcctgcaccaggactggctgaatggcaaggag tacaagtgcaaggtctccaacaaagccctcccagccccatcgagaaaacaatctccaaagccaaagggcagccccgagaacc agcgacatcgccgtggagtgggagagcaatgggcagccggagaacaactacaagaccacgcctcccgtgctggactccgacgget cette tte cteta cage a agete aceg tgg a caa gage aget gg cage ageg gg a aegtet te te at get ceg tgg at geat gage ageg gg a aegtet te te at get ceg tgg at geat gage ageg gg a aegtet te te at get ceg tgg at geat gage ageg gg a aegtet te te at get ceg tgg at geat gage ageg gg a aegtet te te at get ceg tgg at geat gg at geat gg at geat gage ageg gg a aegtet te te at get ceg tgg at geat gage ageg gg a aegtet te te at get ceg tgg at geat gg at gg at geat gg at gg at geat gg at geat gg at gg atgetetgeacaaceactacaegeagaagageeteteeetgteteegggtaaatgatetaga